

181547

115

STIC-Biotech/ChemLib

From: Ibrahim, Medina A.  
Sent: Tuesday, March 07, 2006 10:40 AM  
To: STIC-Biotech/ChemLib  
Subject: 10/656,394

RECEIVED  
MAR - 7 2006  
STIC

Please do an interference search of the following:

1. DNA encoding SEQ ID NO: 8.
2. SEQ ID NO: 7. Thanks

Medina A. Ibrahim  
Patent Examiner, GAU-1638  
transgenic plants and plant breeding  
Remsen-2B07  
mailbox-2C18  
(571) 272-0797

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

Mon Mar 13 10:28:19 2006

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 18:59:29 ; Search time 531 Seconds  
(without alignments)  
10374.131 Million cell updates/sec

Title: US-10-656-394A-7  
Perfect score: 3099  
Sequence: 1 atggcgagacgtgtgag.....gcacagctcaagctgctga 3099

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/ina/1 COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/ina/PP COMB.seq:\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq:\*
- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122.6	4.0	3925	US-09-330-330-2	Sequence 2, Appli
2	106.6	3.4	10322	US-09-330-330-3	Sequence 3, Appli
3	81.6	2.6	5113	US-09-336-9468-3	Sequence 3, Appli
4	81.6	2.6	5222	US-09-336-9468-68	Sequence 68, Appli
5	81.6	2.6	5222	US-09-993-170-57	Sequence 57, Appli
6	81.6	2.6	5696	US-09-993-170-60	Sequence 60, Appli
7	81.6	2.6	5757	US-09-336-9468-1	Sequence 1, Appli
8	81.6	2.6	5757	US-09-993-170-56	Sequence 56, Appli
9	62.6	2.0	2718	US-09-360-186-4	Sequence 4, Appli
10	62.6	2.0	2718	US-09-864-680A-4	Sequence 4, Appli
11	62.6	2.0	3099	US-09-360-186-2	Sequence 2, Appli
12	62.6	2.0	3099	US-09-864-680A-2	Sequence 2, Appli
13	62.6	2.0	31491	US-09-360-186-1	Sequence 1, Appli
14	62.6	2.0	31491	US-09-864-680A-1	Sequence 1, Appli
15	57.4	1.9	3997	US-08-947-823-2	Sequence 2, Appli
16	57.4	1.9	51952	US-08-947-823-1	Sequence 1, Appli
17	52.8	1.7	5475	US-08-680-327-1	Sequence 1, Appli
18	52.8	1.7	5475	US-09-228-246-3	Sequence 3, Appli
19	52.8	1.7	10968	US-08-680-327-2	Sequence 2, Appli
20	52.8	1.7	10968	US-09-228-246-1	Sequence 1, Appli
21	50.6	1.6	4946	US-08-930-996A-1	Sequence 1, Appli
22	50.4	1.6	7218	US-08-232-463-14	Sequence 14, Appli
23	49.8	1.6	4163	US-09-004-838-70	Sequence 70, Appli
24	49.8	1.6	4208	US-09-004-838-1	Sequence 1, Appli

25	49.4	1.6	3982	3	US-08-947-823-4	Sequence 4, Appli
26	49.4	1.6	9870	3	US-09-245-928A-15	Sequence 15, Appli
27	49	1.6	3741	3	US-09-803-286A-1	Sequence 1, Appli
28	46.6	1.5	1662	3	US-09-004-838-6	Sequence 6, Appli
29	46.2	1.5	2353	3	US-09-004-838-2	Sequence 2, Appli
30	45.4	1.5	1141	3	US-09-806-708B-22	Sequence 22, Appli
31	44.2	1.4	3635	2	US-08-588-983-15	Sequence 15, Appli
32	44.2	1.4	3635	2	US-08-588-976-15	Sequence 15, Appli
33	43.8	1.4	1141	3	US-09-806-708B-22	Sequence 22, Appli
34	43.6	1.4	5134	3	US-08-310-912A-157	Sequence 157, App
35	43.6	1.4	5134	3	US-09-301-085-157	Sequence 157, App
36	43.6	1.4	5134	6	PCT-US95-04589-157	Sequence 3, Appli
37	40.6	1.3	1036	3	US-09-004-838-3	Sequence 128, App
38	40.2	1.3	1038	3	US-09-004-838-128	Sequence 2813, Ap
39	39.8	1.3	832	3	US-09-621-976-2813	Sequence 2813, Ap
40	39	1.3	832	3	US-09-621-976-2813	Sequence 109, App
41	38.4	1.2	5829	3	US-09-004-838-109	Sequence 16369, A
42	38.4	1.2	136917	3	US-09-949-016-16369	Sequence 7366, Ap
43	38	1.2	478	3	US-09-270-767-7366	Sequence 22648, A
44	38	1.2	478	3	US-09-270-767-22648	Sequence 33950, A
45	38	1.2	601	3	US-09-949-016-33950	

## ALIGNMENTS

## RESULT 1

US-09-330-330-2

/ Sequence 2, Application US/09330330

/ Patent No. 6274789

/ GENERAL INFORMATION:

/ APPLICANT: Yano, Masahiro

/ APPLICANT: Iwamoto, Masao

/ APPLICANT: Katayose, Yuichi

/ APPLICANT: Sasaki, Takuji

/ APPLICANT: Wang, Zi-Xuan

/ APPLICANT: Yamanouchi, Utako

/ APPLICANT: Ishimaru, Lisa

/ TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE

/ NUMBER OF SEQUENCES: 13

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Fish & Richardson P.C.

/ STREET: 225 Franklin Street

/ CITY: Boston

/ STATE: MA

/ COUNTRY: USA

/ ZIP: 02110-2804

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Diskette

/ COMPUTER: IBM Compatible

/ OPERATING SYSTEM: DOS

/ SOFTWARE: FastSeq for Windows Version 2.0

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/330,330

/ FILING DATE: 11-JUN-1999

/ PRIORITY APPLICATION DATA:

/ APPLICATION NUMBER: JP 10-181455

/ FILING DATE: 12-JUN-1998

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Fraser, Ph.D., J.D., Janis K.

/ REGISTRATION NUMBER: 34,819

/ REFERENCE/DOCKET NUMBER: 06501/032001

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: 617/542-5070

/ TELEFAX: 617/542-8906

/ INFORMATION FOR SEQ ID NO: 2:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 3925 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: double

/ TOPOLOGY: linear

/ MOLECULE TYPE: cDNA to mRNA

/ FEATURE:



Db 7087 GCAATAGTTGCTAGTGGTATCTTTGGCAAAACCGACCAAGACCCCAAGAGAGTGGAGA 7146  
Qy 1186 AAATTTCTATGAACACCTTCCTTCAGAACTAGAAATAAACCACCGCTCGAGCTTTCAGG 1245  
Db 7147 AAATTTGAACGAGATATCAATGCTGAGTTGGAATGAAATCCAGAGCTTGGATATAGA 7206  
Qy 1246 AGAATGGTACCTTAGGTATCAACACCTACATCCATCCATTTGAACCAAGCTTTTGTAT 1305  
Db 7207 ACCGCTCTTGAAAAAGCTATGATGTTTACCATACCATCTCAAGCTCATGTTTTTATAT 7266  
Qy 1306 CTAAGTATCTTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGATA 1365  
Db 7267 CTGTCCATTTTCCCTGAGACCATGATTTAGTCGAGGCGTTTGGTGCATCGTTGGCA 7326  
Qy 1366 CGAAGGGTTTGTAGACCAAGGTGGGATGACGACTAAGGATGTTCGGAAGAAAGTTAC 1425  
Db 7327 GCAGAAGTTACTCAATCGACGACATCGCAATCTGCCATTTGAAATAGCTAACGGCTAC 7386  
Qy 1426 TTTAATGAGCTATCAACCAAGTATGATTTCAAGAT-----CAAGAGTGGCATGCA 1479  
Db 7387 TTTAATGAGCTATCAACCAAGTATGATTTCAAGAT-----CAAGAGTGGCATGCA 1479  
Qy 1480 GGAATAATTAAGACTTGTGCAATTCATGATATCATCGTGATATCACAAGTTTCAATCTCG 1539  
Db 7447 AAATCAATGACTCTTGCAAGTCCATGATCTCATGCGTGACATCGCCATCTCAAGTCA 7506  
Qy 1540 AGACAGGAAATTTGTATTTATTAACCAATGGGAGATGGCTGTGATTTAGTTTCAAGAAAC 1599  
Db 7507 ACGGAGAAACCTTTGTTTGGGTGGAGGAGGCTGCGCGGTACATACATGATGGTCA 7566  
Qy 1600 ACTCGCACATAGCATTTCCATGGGAGTATGCTCGCAAACTGGGATTTGGATGGAGCAT 1659  
Db 7567 ATTGCTCATCTTGTCTAATGCAACTGGAAGGAGATAGAGTGAATTCGAGGCGATA 7626  
Qy 1660 ATTGCTCATCTTGTCTAATGCAACTGGAAGGAGATAGAGTGAATTCGAGGCGATA 1719  
Db 7627 GTGACCTGTCCCGAATACATCGTTATCTCTGTTTGGGGATTTGGAAGCCATTTTGT 7686  
Qy 1720 GATCAATTTGAGGATTTTACGGGTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAA 1779  
Db 7687 TATGCAAGATGAGTTTATACAGTGTCTTGAAGGAGTGTGAGGCTAGAGGCTAGATAT 7746  
Qy 1780 AAGATTTGACCGTATGATGTTTGTGCGACTTGAATATCTGAGTATGGATTTG 1839  
Db 7747 CATCACTTGTAGATTTGGAAGCTTAATCACTTAAATTTCTTCTACGAGGATG 7806  
Qy 1840 TCATCCATATATTCATCTCCAGATCCATTTGGTAAACTACAGGGCTACAACTTTGAAC 1899  
Db 7807 TATCGTATGATCTGACAGATTTTACGCGACCTGAGGCACTCCAGATGCTAGAC 7866  
Qy 1900 ATGCGGAGCATATCATTTGAGCAGCATACCAAGTATGATGATTAATCTCAATGCTGCAT 1959  
Db 7867 ATCAGAGTATATATGTAAGGCTTTGCCAAAAAACCATCATCAAGCTTTCAGAGCTACAG 7926  
Qy 1960 ACTCTTCGT 1968  
Db 7927 TACATTCAT 7935

RESULT 3  
US-09-336-946B-3  
; Sequence 3, Application US/09336946B  
; Patent No. 6479731  
; GENERAL INFORMATION:  
; APPLICANT: Valent, Barbara S.  
; APPLICANT: Bryan, Gregory  
; APPLICANT: E. I. du Pont de Nemours and Company  
; TITLE OF INVENTION: A PI-TA GENE CONFERRING DISEASE RESISTANCE TO PLANTS  
; FILE REFERENCE: BB-1136  
; CURRENT APPLICATION NUMBER: US/09/336, 946B  
; PRIORITY FILING DATE: 1999-06-21  
; PRIORITY FILING DATE: 1999-06-21  
; PRIORITY FILING DATE: 1999-06-21

Qy 908 ACATTAAGAGGCGAGTCCGAATAGTAATAACCACTCGGAATGTTGATCTTCGCGAGAAGT 967  
Db 3124 ATAATAATAGTTGCGATAGTAATAATAACCAAGAAATTTGAACCTGTAGCTTTGGCAT 3183  
Qy 968 GTGCCACAGCCTCACTGGTGTACCACTTTGATTTCTTCAGATGAACGATGCCAATAACAT 1027  
Db 3184 GCTGTGATATACTCAGAGCACATTTATAGATTGATCCACTGGGTGATGATGCTCAA 3243  
Qy 1028 TGCTACTGAGAAACAAATAAATCATGAGACATGGAATCAATAAATAAATAATGCAAA 1087  
Db 3244 GTCAATTTGTTTTCAGTGGAGTTGTTGGCAAGGAATGAATTTCTCGGACATTTACTG 3303  
Qy 1088 AGATGGTTGAACCAATTTGTAATAAATGTTGCTCTACCATTTAGCAATATCTTACAATAG 1147  
Db 3304 AAGTTTCTCATGACATGATAAATAATGTTGGCTTGGCTGCCACTAGCAATACTATAACAG 3363  
Qy 1148 GAGCTGTGCTTGAACCAATGAGGTGTGAGATGGGAGAAATTTCTATGAACACTT----- 1202  
Db 3364 CCAGACATTTTAAAGCCAGCTGTTAGATGGAATGCAATGGAATCAATACATAAATAAT 3423  
Qy 1203 -----TCCTTCAGAACTAGAAATAAACCAGCTTGAAGCTTTGAGGAGATGTTGA 1255  
Db 3424 CATTGACTACTTCCATTTGAAGAAATCTTACTTTGCGAGGATGAGCAAGTACTCA 3483  
Qy 1256 CCTAGGTATCAACACCTACCATCCCATTTGAAACCAATGCTTTTGTATCTAAGTATCT 1315  
Db 3484 ACCTTATTTACATATCTTCTCTCAATGTTTGAAGCATGCTGTATATACCTTTAGCATCT 3543  
Qy 1316 TTCTGAGGATTTTGAATAAATAAAGCAATCGTCTAGTAGTGTAGATGATGATGAGCAAGG 1375  
Db 3544 ACAAGAGGCTACATAATTTAGAGGCGCACTTTGTTGAGGCAATGATGCTGAGGTT 3603  
Qy 1376 TTGTTAGACCAAGGTTGGGATGAGCATTAAGATGTCGAGAGAAAGTTACTTTAATGAGC 1435  
Db 3604 TCATCAATTCATAGAAAAATAAAGTCATGGAAGAGTTGCGAGGAACTATTTTGTGATGAC 3663  
Qy 1436 TAATCAACCGAGTATGATTTCAACCATCAAGAGTGGGCATAGCAGGAAAAAATAAGACTT 1495  
Db 3664 TTGTTGTTAGGGGCTGCTCCAACTAGATGTTAATCTGCAAAATGAGGATTTGTCAT 3723  
Qy 1496 GTGCAATTTCAATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAGGAAAAATTT 1553  
Db 3724 GTGTAGTGCACCATGTTTAAATTTTATGAGTGTAAAGTCAATAGAGGAGAAATTT 3781

RESULT 4  
US-09-336-946B-68  
; Sequence 68, Application US/09336946B  
; Patent No. 6479731  
; GENERAL INFORMATION:  
; APPLICANT: Valent, Barbara S.  
; APPLICANT: Bryan, Gregory  
; APPLICANT: E. I. du Pont de Nemours and Company  
; TITLE OF INVENTION: A PI-TA GENE CONFERRING DISEASE RESISTANCE TO PLANTS  
; FILE REFERENCE: BB-1136  
; CURRENT APPLICATION NUMBER: US/09/336, 946B  
; PRIORITY FILING DATE: 1999-06-21  
; PRIORITY FILING DATE: 1999-06-21  
; PRIORITY FILING DATE: 1999-06-21  
; PRIORITY FILING DATE: 1999-06-21  
; PRIORITY FILING DATE: 1999-06-21



SOFTWARE: Microsoft Office 97  
SEQ ID NO 68  
LENGTH: 5222  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-09-993-170-57

Query Match 2.6%; Score 81.6; DB 3; Length 5222;  
Best Local Similarity 46.7%; Pred. No. 1.1e-13;  
Matches 307; Conservative 0; Mismatches 339; Indels 12; Gaps 1;  
QY 908 ACAATAGAGGGGAGTCGAATAGTAATTAACCACTCGGAATGTTGATCTTCGGGAGAAGT 967  
DB 3438 ATAATAATAGTTGCGAGTAGAATACTAATAACCAAGAAATGAACTGTAGCTTTGGCAT 3497  
QY 968 GTGCCACAGGCTCACTGGTGTACCACTTTGATTTCTTGAGATGAACGATGCCATAACAT 1027  
DB 3498 GCTGTGATATACTCAGACACATTAATTAAGATTGATCCACTGGGTGATGATGCTCAA 3557  
QY 1028 TGCTACTGAGAAAACAAATAAATAATCATGAGACATGGAATCAAAATAAATAATGCAAA 1087  
DB 3558 GTCAATTTGTTTTTCAGTGGAGTTGTTGGCCAAAGAAATGAATTTCTTGACATCTTACTG 3617  
QY 1088 AGATGGTTGAACGAATTTGTAATAAATGTTGCTCTACCATTTAGCAATCTTACATAG 1147  
DB 3618 AAGTTTCTCATGATGATTAATAAATGTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 3677  
QY 1148 GAGCTGTGCTTGGCACTAAACAGGTGTGAGATGGGAGAAATTTCTATGAACACCT----- 1202  
DB 3678 CCAGACATTTTAAAGCCAGCTGTTAGATGGAATGCAATGGAATCACAACAATAAAT 3737  
QY 1203 -----TCCTTCAGAACTAGAAATAAACCAGCCTGGAAGCTTTGAGGAGAAATGTTGA 1255  
DB 3738 CATTTGACTACTTCCATTTTGAAGAAATTCCTACTTTTCAGGGGATGAGGCAAGTACTCA 3797  
QY 1256 CCCTAGGTTACACCACTTACCATCCCATTTTGAACCAATGCTTTTGTATCTAAGTATCT 1315  
DB 3798 ACCTTATTTACAAATAATCTTCTCTCATTTGTTTGAAGCAATGCTGTTATACCTTAGCATCT 3857  
QY 1316 TTCTGAGGATTTTGAATCAAAAGGAATTCGCTAGTAGGTAGATGATAGCAGAGGTT 1375  
DB 3858 ACAAGAGGACTACATAATATTAGGAAGGCCAATCTTGGTGAGCAATGAGTGCCTGAAGTT 3917  
QY 1376 TTGTTAGACCAAGGTTGGGATGACGACTAAGATGTCGGAAGATTTACTTTAATGAGC 1435  
DB 3918 TCATCAATTCATAGAAAATAAAGTCATGGAAGATTTGCAAGGAACTATTTTGAATGAAC 3977  
QY 1436 TAATCAACCGAATGATGATTTCAACGATCAAGATGGGATGAGTGAAGAAATTAAGACTT 1495  
DB 3978 TTGTTGTTAGGGGCTGGTCCCAACAGTAGATGTTAACTGCAAAAATGAGGTATTGTCTAT 4037  
QY 1496 GTCGAATTCATGATATCATCCGCTGATATCAGATTTCAATCTCGAGACAGGAAATTT 1553  
DB 4038 GTGTAGTGCACCATGTTTAAATTTTCAATCAGGTGTAAGTCAATAGAGGAGAAATTT 4095

## RESULT 5

US-09-993-170-57  
Sequence 57, Application US/09993170  
Patent No. 6743969  
GENERAL INFORMATION:  
APPLICANT: Valent, Barbara  
APPLICANT: Bryan, Gregory  
TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene  
TITLE OF INVENTION: Specificity and Method for Engineering Altered  
TITLE OF INVENTION: Specificity  
FILE REFERENCE: BB1385 US NA  
CURRENT APPLICATION NUMBER: US/09/993,170  
CURRENT FILING DATE: 2001-11-26  
PRIOR APPLICATION NUMBER: 60/248,335  
PRIOR FILING DATE: 2000-11-14  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: Microsoft Office 97

SEQ ID NO 57  
LENGTH: 5222  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-09-993-170-57

Query Match 2.6%; Score 81.6; DB 3; Length 5222;  
Best Local Similarity 46.7%; Pred. No. 1.1e-13;  
Matches 307; Conservative 0; Mismatches 339; Indels 12; Gaps 1;  
QY 908 ACATAGAGGGGAGTCGAATAGTAATTAACCACTCGGAATGTTGATCTTCGGGAGAAGT 967  
DB 3438 ATAATAATAGTTGCGAGTAGAATACTAATAACCAAGAAATGAACTGTAGCTTTGGCAT 3497  
QY 968 GTGCCACAGGCTCACTGGTGTACCACTTTGATTTCTTGAGATGAACGATGCCATAACAT 1027  
DB 3498 GCTGTGATATACTCAGACACATTAATTAAGATTGATCCACTGGGTGATGATGCTCAA 3557  
QY 1028 TGCTACTGAGAAAACAAATAAATAATCATGAGACATGGAATCAAAATAAATAATGCAAA 1087  
DB 3558 GTCAATTTGTTTTTCAGTGGAGTTGTTGGCCAAAGAAATGAATTTCTTGACATCTTACTG 3617  
QY 1088 AGATGGTTGAACGAATTTGTAATAAATGTTGCTCTACCATTTAGCAATCTTACATAG 1147  
DB 3618 AAGTTTCTCATGATGATTAATAAATGTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 3677  
QY 1148 GAGCTGTGCTTGGCACTAAACAGGTGTGAGATGGGAGAAATTTCTATGAACACCT----- 1202  
DB 3678 CCAGACATTTTAAAGCCAGCTGTTAGATGGAATGCAATGGAATCACAACAATAAAT 3737  
QY 1203 -----TCCTTCAGAACTAGAAATAAACCAGCCTGGAAGCTTTGAGGAGAAATGTTGA 1255  
DB 3738 CATTTGACTACTTCCATTTTGAAGAAATTCCTACTTTTCAGGGGATGAGGCAAGTACTCA 3797  
QY 1256 CCCTAGGTTACACCACTTACCATCCCATTTTGAACCAATGCTTTTGTATCTAAGTATCT 1315  
DB 3798 ACCTTATTTACAAATAATCTTCTCTCATTTGTTTGAAGCAATGCTGTTATACCTTAGCATCT 3857  
QY 1316 TTCTGAGGATTTTGAATCAAAAGGAATTCGCTAGTAGGTAGATGATAGCAGAGGTT 1375  
DB 3858 ACAAGAGGACTACATAATATTAGGAAGGCCAATCTTGGTGAGCAATGAGTGCCTGAAGTT 3917  
QY 1376 TTGTTAGACCAAGGTTGGGATGACGACTAAGATGTCGGAAGATTTACTTTAATGAGC 1435  
DB 3918 TCATCAATTCATAGAAAATAAAGTCATGGAAGATTTGCAAGGAACTATTTTGAATGAAC 3977  
QY 1436 TAATCAACCGAATGATGATTTCAACGATCAAGATGGGATGAGTGAAGAAATTAAGACTT 1495  
DB 3978 TTGTTGTTAGGGGCTGGTCCCAACAGTAGATGTTAACTGCAAAAATGAGGTATTGTCTAT 4037  
QY 1496 GTCGAATTCATGATATCATCCGCTGATATCAGATTTCAATCTCGAGACAGGAAATTT 1553  
DB 4038 GTGTAGTGCACCATGTTTAAATTTTCAATCAGGTGTAAGTCAATAGAGGAGAAATTT 4095

## RESULT 6

US-09-993-170-60  
Sequence 60, Application US/09993170  
Patent No. 6743969  
GENERAL INFORMATION:  
APPLICANT: Valent, Barbara  
APPLICANT: Bryan, Gregory  
TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene  
TITLE OF INVENTION: Specificity and Method for Engineering Altered  
TITLE OF INVENTION: Specificity  
FILE REFERENCE: BB1385 US NA  
CURRENT APPLICATION NUMBER: US/09/993,170  
CURRENT FILING DATE: 2001-11-26  
PRIOR APPLICATION NUMBER: 60/248,335  
PRIOR FILING DATE: 2000-11-14  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 60

; LENGTH: 5696

; TYPE: DNA  
; ORGANISM: Artificial Sequence; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Chimeric Gene  
US-09-993-170-60

Query Match 2.6%; Score 81.6; DB 3; Length 5696;  
Best Local Similarity 46.7%; Pred. No. 1.2e-13;  
Matches 307; Conservative 0; Mismatches 339; Indels 12; Gaps 1;

Qy 908 ACAATAAGAGGGCAGTCGAATAGTAATAACACCTCGGAATGTTGATCTTCGGGAGAAGT 967  
Db 3438 ATAATAATAGTTGCACTAGATAGTAATAACACCTCGGAATGTTGATCTTCGGGAGAAGT 967

Qy 968 GTGCCACAGCCTCAGTGTGTTACCACTTGTCTTTCGAGATGAAGATGCCATAACAT 1027  
Db 3498 GCTGTGGATATACTCAGAGCACATTTAAGATTGATCCACTGGGTGATGATGCTCAA 3557

Qy 1028 TGCTACTGAGAAAACAAATATAAATCATGAAGACATGGAATCAAAATAAATAATGCAA 1087  
Db 3558 GTCAATTTGTTTTCAGTGGAGTTGTTGGCCAAAGGAATGAATTTCTTGGACATCTTACTG 3617

Qy 1088 AGATGGTTGAACGAATGTAAATPAATGTGGTCTACCACTAGCAATATCTTCAATAG 1147  
Db 3618 AAGTTTCTCATGATGATATAAATAATGTGGTGGCTTGCCTAGCAATATCTTCAACAG 3677

Qy 1148 GAGCTGTGCTTGCACACTTAACAGGTGTCAAGATGGGAGAAATCTTATGAACACCT 1202  
Db 3678 CCAGACATTTTAAAGCCAGCTGTATAGATGGATGCGATGGAATCATACAAAAT 3737

Qy 1203 -----TCCTTCAGAACTAGAAAATAAACCCAGCTGGAAGCTTTTGAGGAGAATGTGA 1255  
Db 3738 CATTGACTACTTCCAAATTTGAAGAAAATCTTACTTTGAGGGGATGAGGCAAGTACTCA 3797

Qy 1256 CCCTAGGTACACCACTACCATCCATTTGAAACCACTGCTTTTGTATCTAGATATCT 1315  
Db 3798 ACCTATTATCAATAATCTTCTCATTTGTTGAAAGCATGCTGTATACCTTAGCATCT 3857

Qy 1316 TTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGTAGTAGTAGTAGTAGTAGT 1375  
Db 3858 ACAAGAGGACTACATAATTTAGGAGGCCAATTTGTTGAGGCAATGGATGCTCAAGGTT 3917

Qy 1376 TTGTTAGACCAAGTTGGATGACACTAAGATGTCGAGAGAAATTTTAAATGAGC 1435  
Db 3918 TCATCAATCCAGATTTGGATGACACTAAGATGTCGAGAGAAATTTTAAATGAGC 3977

Qy 1436 TAATCAACCGAAGTATGATTTCAACGATCAAGATGTCGAGAGAAATTTTAAATGAGC 1495  
Db 3978 TTGTTGTTAGGGGCTGCTCAACAGTAGATGTTAACTGCAAAAATGAGGTATTTGTCAT 4037

Qy 1496 GTCGAATTCATGATATATCATCCGATATCAGAGTTTCAATCTCGAGACAGGAAATTT 1553  
Db 4038 GTGTAGTGCCACCATGTTATTAATTTTCAATCAGGTGAAGTCAATAGAGGAGAATTT 4095

## RESULT 7

US-09-336-946B-1

; Sequence 1, Application US/09336946B

; Patent No. 6479731

; GENERAL INFORMATION:

; APPLICANT: Valent, Barbara S.

; APPLICANT: Bryan, Gregory

; APPLICANT: E. I. du Pont de Nemours and Company

; TITLE OF INVENTION: A P-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS

; FILE REFERENCE: BB-1136

; CURRENT APPLICATION NUMBER: US/09/336, 946B

; PRIOR FILING DATE: 1999-06-21

; PRIOR APPLICATION NUMBER: 60/095229

; PRIOR FILING DATE: 1998-08-04

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 1

; LENGTH: 5757

; TYPE: DNA  
; ORGANISM: Oryza sativa

US-09-336-946B-1

Query Match 2.6%; Score 81.6; DB 3; Length 5757

Best Local Similarity 46.7%; Pred. No. 1.2e-13;

Matches 307; Conservative 0; Mismatches 339; Indels 12; Gaps 1;

Qy 908 ACAATAAGAGGGCAGTCGAATAGTAATAACACCTCGGAATGTTGATCTTCGGGAGAAGT 967  
Db 3731 ATAATAATAGTTGCACTAGATAGTAATAACACCTCGGAATGTTGATCTTCGGGAGAAGT 967

Qy 968 GTGCCACAGCCTCAGTGTGTTACCACTTGTCTTTCGAGATGAAGATGCCATAACAT 1027  
Db 3791 GCTGTGGATATACTCAGAGCACATTTAAGATTGATCCACTGGGTGATGATGCTCAA 3850

Qy 1028 TGCTACTGAGAAAACAAATATAAATCATGAAGACATGGAATCAAAATAAATAATGCAA 1087  
Db 3851 GTCAATTTGTTTTCAGTGGAGTTGTTGGCCAAAGGAATGAATTTCTTGGACATCTTACTG 3910

Qy 1088 AGATGGTTGAACGAATGTAAATPAATGTGGTCTACCACTAGCAATATCTTCAATAG 1147  
Db 3911 AAGTTTCTCATGATGATATAAATAATGTGGTGGCTTGCCTAGCAATATCTTCAACAG 3970

Qy 1148 GAGCTGTGCTTGCACACTTAACAGGTGTCAAGATGGGAGAAATCTTATGAACACCT 1202  
Db 3971 CCAGACATTTTAAAGCCAGCTGTATAGATGGATGGAATCATACAAAAT 4030

Qy 1203 -----TCCTTCAGAACTAGAAAATAAACCCAGCTGGAAGCTTTTGAGGAGAATGTGA 1255  
Db 4031 CATTGACTACTTCCAAATTTGAAGAAAATCTTACTTTGAGGGGATGAGGCAAGTACTCA 4090

Qy 1256 CCCTAGGTACACCACTACCATCCATTTGAAACCACTGCTTTTGTATCTAGATATCT 1315  
Db 4091 ACCTATTATCAATAATCTTCTCATTTGTTGAAAGCATGCTGTATACCTTAGCATCT 4150

Qy 1316 TTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGTAGTAGTAGTAGTAGTAGT 1375  
Db 4151 ACAAGAGGACTACATAATTTAGGAGGCCAATTTGTTGAGGCAATGGATGCTCAAGGTT 4210

Qy 1376 TTGTTAGACCAAGTTGGATGACACTAAGATGTCGAGAGAAATTTTAAATGAGC 1435  
Db 4211 TCATCAATCCAGATTTGGATGACACTAAGATGTCGAGAGAAATTTTAAATGAGC 4270

Qy 1436 TAATCAACCGAAGTATGATTTCAACGATCAAGATGTCGAGAGAAATTTTAAATGAGC 1495  
Db 4271 TTGTTGTTAGGGGCTGCTCAACAGTAGATGTTAACTGCAAAAATGAGGTATTTGTCAT 4330

Qy 1496 GTCGAATTCATGATATATCATCCGATATCAGAGTTTCAATCTCGAGACAGGAAATTT 1553  
Db 4331 GTGTAGTGCCACCATGTTATTAATTTTCAATCAGGTGAAGTCAATAGAGGAGAATTT 4388

## RESULT 8

US-09-993-170-56

; Sequence 56, Application US/09993170

; Patent No. 6743969

; GENERAL INFORMATION:

; APPLICANT: Valent, Barbara

; APPLICANT: Bryan, Gregory

; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene

; TITLE OF INVENTION: Specificity and Method for Engineering Altered

; TITLE OF INVENTION: Specificity

; FILE REFERENCE: BB1385 US NA

; CURRENT APPLICATION NUMBER: US/09/993,170

; PRIOR FILING DATE: 2001-11-26

; PRIOR APPLICATION NUMBER: 60/248,335

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 56

; LENGTH: 5757

```

; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-993-170-56

Query Match      2.6%; Score 81.6; DB 3; Length 5757;
Best Local Similarity 46.7%; Pred.No.1.2e-13;
Matches 307; Conservative 0; Mismatches 339; Indels 12; Gaps 1;

QY  908 ACAATAAGACGGCAGTCGAATAGTAATACCACTCGAATGTCATCTCCGGAGAAGT 967
DB  7331 ATNATNATGTGAGTAGATACTAATAACAACAGAAATGAACCTGTAGCTTTGCCAT 3790
QY  968 GTGCACAGCCTCACTGGTGACACCCTTGATTTCTTGAGATGAACGATGCCATAACAT 1027
DB  3791 GCTGTGGATATAAATCTCAGACGACATATTATTAAGATTGATCCACTGGGTGATGCTCAA 3850
QY  1028 TGCTACTCAGAAAAACAAAATAAATCATGACGACATGAATCAAAATAAAAAATATGCAA 1087
DB  3851 GTCAATGTGTTTTCACTGGAGTGTGTCGCCAGGAATGAATTTCTTGGCACATCTTACTG 3910
QY  1088 AGATGGTTGAACGAATTTGTAATAATATGCTGCTTACCATAGCAATATCTTACATAG 1147
DB  3911 AAGTTTCTCATGACATGATAAAAAATATGCTGGCTTGGCCACTAGCAATAACTATAACAG 3970
QY  1148 GAGCTGTGCTTGCACACTAAACAGCTGTGAGATGGGAGAAATTTCTATCAACACCT --- 1202
DB  3971 CAGACATTTTAAAGCCAGCTGTAGATGGAATGCGAATGGAAATCACATACAAAAT 4030
QY  1203 -----TCCTTCAGAACTAGAAATAAACCAAGCCTGGAAGCTTTTGAGGAGATGGTGA 1255
DB  4031 CATTGACTACTTCCAATTTGAAAGAAAATCCTACTTTTGCAGGGGATGAGGCAAGTACTCA 4090
QY  1256 CCTAGGTTTCAACACCTACCTACCTCCATTTGAAACCATGCTTTTGTATCTAAGATATCT 1315
DB  4091 ACCATTATTAACAATATCTTCTCATGTTTGAAGCAATGCTGTATATACCTTAGCATCT 4150
QY  1316 TTCTCGAGATTTGAAATCAAAAGGAATCGCTAGTAGTAGTAGATGATAGCAGAGGT 1375
DB  4151 ACMAAGAGGACTACATAATATTAGGAGGCCAACTTTGTGAGGCAANTGGATGGCTGAAGGT 4210
QY  1376 TTGTTAGACCAAGGTTGGGATGACGACTAAGGATGCGGAGAAAGTTACTTTAATGAGC 1435
DB  4211 TCATCAATTCATAGAAAATAAAGTCATGGAAGAAGTTCAGGGAACACTATTTTGATGAAC 4270
QY  1436 TAATCAACGGAAGTATGATTCACGATCAAGATGGGATGCGCATACAGAAAATTAAGCTT 1495
DB  4271 TTGTTGGTAGGGGCTTGGTCCACCAAGTAGATGTTAACTGCAAAAATGAGGTATTGTCAT 4330
QY  1496 GTCCGAATTCATGATATCATCCGTGATATCAAGTTTCAATCTCCGAGACAGGAAAATTT 1553
DB  4331 GTGTAGTCACCACTGTTATTAATTTTCATCAGGTGTAAGTCAATAGAGGAGAATTT 4388

RESULT 9
US-09-360-186-4
; Sequence 4, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, et al.
; TITLE OF INVENTION: B2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; EARLIER FILING DATE: 1999-07-23
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2718
; TYPE: DNA
; ORGANISM: Capsicum annuum
; FEATURE:
; NAME/KEY: CDS

Query Match      2.0%; Score 62.6; DB 3; Length 2718;
Best Local Similarity 47.2%; Pred.No.5.7e-08;
Matches 265; Conservative 0; Mismatches 284; Indels 12; Gaps 2;

QY  821 TCAAGGAGAGAGGTACTTTTGTGTTCTAGATGATCTATGATTTTACATGATTTGGAATT 880
DB  755 TAAAGAGAAAGAGGTACTTTAAATTGTTCTGGATGATATCTGGAGTTGTGAAGTGTGGGATG 814
QY  881 GGATAAATGAATTTGCATTTCCCTAAGAACAAATAAGAGGCGAGTCGAATAGTAATACCA 940
DB  815 GCGTGA---GACATGCTCTTCCAACTGAAGCAATGCGAGGAGTCGAATACTTGTGACTA 871
QY  941 CTGGAATGTTGATCTTTGCGGAGAAAGTGTGCCACAGCCTCACTCGTGTACACCTTGAAT 1000
DB  872 CCCGTAATGATGAAGTAGCTTGTATGCTGGTGTAGAGAAATTTTCTTTTTCGGATGAGCT 931
QY  1001 TCTTGAGATGACGATGCCATAACATTTGCTACTCTGAGAAAACAAAATAAAATCATGAAG 1060
DB  932 TCATGGATCAAGATGAGAGTTGGAGTCTTTTCAAAAGTGCAGCAATTTTCAAGTGA --- 986
QY  1061 ACATGGAATCAAAATAAAAAATATGCAAAAGATGGTTGAAACGAATTTGTAATAAATGTGGTC 1120
DB  987 ----AGCATTTACCATATGATGTTTCGAGACTGTTTGGAAAGCAAAATCGCAGATGAATGTCA 1042
QY  1121 GTCTACCATTTAGCAATTAACATAGAGGAGTGTCTTGCCTCACTAAACAGGTGTCAGAAAT 1180
DB  1043 GGTTCACCACTAACTATTTGCTGGTGTGACAGGCTTCTCAATCTAAAGAGCAATAGAG 1102
QY  1181 GGGAGAAATTTATAGAACACCTTCTCTTCCAGAACTAGAAAATAAAACCAAGCCTGGAAGCTT 1240
DB  1103 ATTGAAAACTGTTGCTAAAGATGTCAAGTCACTTCGTCAAAATGATCCTGATGAACGAT 1162
QY  1241 TGAGGAGAAATGGTGACCTTAGGTACACCACTACCACTACCACTTGAACCACTGCTTTT 1300
DB  1163 GTTCACGTGCTTGGGTTGAGTTAGTACATCTTGACAGGCAATCTAAACATCTCTTC 1222
QY  1301 TGATATCAAGTATCTTTTCTCTGAGGATTTTGAATAATCAAAAGGAATGCTCTAGTAGGTAGAT 1360
DB  1223 TGCATTTTCGGAATTTTTCAGAGAGACAGTGATATTTCCAGTGAAGAAATTTGATGAGATCAT 1282
QY  1361 GGATAGCAGAGAGGTTTGTGTTA 1381
DB  1283 GGATGGCTGAGGGGTTCTCTGA 1303

RESULT 10
US-09-864-680A-4
; Sequence 4, Application US/09864680A
; Patent No. 6762285
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, Brian J
; APPLICANT: Danilbeck, Douglas
; APPLICANT: Tai, Thomas H
; TITLE OF INVENTION: B2 RESISTANCE GENE
; FILE REFERENCE: 42250/234021 (5830-4A)
; CURRENT APPLICATION NUMBER: US/09/864,680A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/360,186
; PRIOR FILING DATE: 1999-07-23
; PRIOR APPLICATION NUMBER: US 60/093,957
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 2718
; TYPE: DNA
; ORGANISM: Capsicum annum
; FEATURE:
; NAME/KEY: CDS

Query Match      2.0%; Score 62.6; DB 3; Length 2718;

```

Best Local Similarity 47.2%; Pred. No. 5.7e-08;		Matches 265; Conservative 0; Mismatches 284; Indels 12; Gaps 2;	
Qy	821	TCAGGAGAGAGGACTTTGTTGTTCTAGATGATCTATGATTTTACATGATTTGGAATT	880
Db	755	TAAAGAGAGAGGACTTTTAAATGTTCTGATGATATCTGAGTTGGAAGTGGGATG	814
Qy	881	GGATAAATGAAATTTGCAATTTCTTAAGAAACAATAAGAGGGCAGTCGAATAGTAACCA	940
Db	815	GCCTGA---GACGATGCTTTCCAACTGAAGACAATGCAGGGAGTCGAATACTGTTGACTA	871
Qy	941	CTCGGATGTTGATCTTGGGAGAGTGTGCCACAGCCTCACTGGTGACCCTTGATT	1000
Db	872	CCCGTAATGATGAAGTAGCTTTGTTATGCTGGTGATAGAAATTTCTTTGGGATGAGCT	931
Qy	1001	TCCTGCAGATGAACGATGCGCAATTAACATTCCTACTGAGAAAAACAATAAATCATGAAG	1060
Db	932	TCATGGATCAAGATGAGAGTTGGAGTCTTTTCAAAGTGCAGCATTTTCAAGTGA-----	986
Qy	1061	ACATGGATCAATAAATAATATGCAAAAGATGTTGACGAATTTGTAATAAATGTCGTC	1120
Db	987	-----AGCAATACCATATGAGTTCCGAGACTGTTGGAAAGCAATCGCAGATGATGTCAAG	1042
Qy	1121	GTCTACCAATAGCAATCTTACAAATAGGAGCTGTGCTTGCACCTAAACAGGTGTGAGAAT	1180
Db	1043	GGTTACCACTAACTATTGTGCTGTTGCAGGGCTTCTCAAATCTAAAGGACAATAGAAAG	1102
Qy	1181	GGGAGAAATTCATGAACACCTTCTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTT	1240
Db	1103	ATTGGAAACTGTGCTAAAGATGTCAAAGTCAATTCGTCAAAATGATCTCTGATGACGAT	1162
Qy	1241	TGAGGAGAAATGGTGACCCCTAGGTTTACAACTACCTACCATCCCATTTGAAACCATGCTTTT	1300
Db	1163	GTTCACGTGTGCTGGGTTGAGTTACGATCACTTGCAAGCGATCTAAACACATGTCTTC	1222
Qy	1301	TGATCTAAGTATCTTCTGAGGATTTTGAATCAAAGGAATCGTCTAGTAGTAGAT	1360
Db	1223	TGCATTTCCGAAATTTTCCAGAAAGACAGTGATATTCAGTGAAGAAATTTGATGAGATCAT	1282
Qy	1361	GGATAGCAGAGGGGTTTGTGA 1381	
Db	1283	GGATGCTGAGGGGTTCTCTGA 1303	
RESULT 11			
US-09-360-186-2			
; Sequence 2, Application US/09360186			
; Patent No. 6262343			
; GENERAL INFORMATION:			
; APPLICANT: Staskiewicz, et al.			
; TITLE OF INVENTION: B2 Resistance Gene			
; FILE REFERENCE: 50687			
; CURRENT APPLICATION NUMBER: US/09/360,186			
; PRIOR FILING DATE: 1999-07-23			
; EARLIER APPLICATION NUMBER: 60/093,957			
; EARLIER FILING DATE: 1998-07-23			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: Patent in Ver. 2.0			
; SEQ ID NO 2			
; LENGTH: 3099			
; TYPE: DNA			
; ORGANISM: Capsicum annuum			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (93)..(2810)			
US-09-360-186-2			
Query Match		2.0%; Score 62.6; DB 3; Length 3099;	
Best Local Similarity 47.2%; Pred. No. 6.3e-08;		Matches 265; Conservative 0; Mismatches 284; Indels 12; Gaps 2;	
Qy	821	TCAAGGAGAGAGGACTTTGTTGTTCTAGATGATCTATGATTTTACATGATTTGGAATT	880

Db 847 TAAAGAGAAAGAGTACTTAATTTCTTGGATGATATCTGGAGTTGTGAAGTGGGATG 906  
QY 881 GGATAATGAAATTCATTTCTTAAGAAACAATAAGAGGCGAGTGCAGATAGTAATAACCA 940  
Db 907 GCGTGA---GACGATGCTTTCCAACTGAAGACAATGACAGGAGTGCAGATAGTGTGACTA 963  
QY 941 CTCGGAATGTTGATCTTGGCGAGAGTGTGCCACAGCCTCACTGGTGTACCACCTTGAT 1000  
Db 964 CCGTATGATGAAGTAGCTTGTATGCTGTGTAGAGAAATTTCTTTCGGATGAGCT 1023  
QY 1001 TCTTGCAGATGAAGTGCAGTAACAATTTGCTACTGAGAAACAACAATAAATCATGAAG 1060  
Db 1024 TCATGGATCAAGATGAGAGTGTGAGTCTTTTCAAAGTGCAGCAATTTTCAAGTGA---- 1078  
QY 1061 ACATGGAAATCAATTAATAATATGCAAAAGATGTTGAACGAATTTGTAATAAATGTTGTC 1120  
Db 1079 ----AGCATTAACATATGAGTTCGAGACTGTTGGAAAGCAATCGCAGATGATGTCAAG 1134  
QY 1121 GTCTACATTAAGCAATTAACAATAAGGAGTGTGCTTGCACCTAAACAGGTGTCAAGAT 1180  
Db 1135 GGTACCACCTAACTATTTGCTGTGTGAGGCTTCTCAAATCTAAAGAGCAATAGAG 1194  
QY 1181 GGGAGAAATCTATGAACACCTTCTTTCAGAACTAGAAATAAACCCAGCCTGGAAGCT 1240  
Db 1195 ATTGAAATCTGTTGCTAAAGATGTCAAGTCAATTCGTCAAAATGATCTGTGATGAT 1254  
QY 1241 TGAGGAGATGTTGACCTTACAGTGTCAACACCTACCATCCCATTTGAAACCATGCTTTT 1300  
Db 1255 GTTACGCTGTGCTGGGTTGAGTTAGGATCACTTGCACAGGATCTAAAGACATGCTTTC 1314  
QY 1301 TGTATCAATGATCTTCTTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGAT 1360  
Db 1315 TGCATTCGGAATTTTCCAGAGACAGTGAATTTCCAGTGAAGATTTGATGATCAT 1374  
QY 1361 GGATGACAGAGGTTTGTGTA 1381  
Db 1375 GGATGGCTGAGGGGTTCTCTGA 1395

RESULT 13  
US-09-360-186-1  
; Sequence 1, Application US/09360186  
; Patent No. 6262343  
; GENERAL INFORMATION:  
; APPLICANT: Staskawicz, et al.  
; TITLE OF INVENTION: B2 Resistance Gene  
; FILE REFERENCE: 50687  
; CURRENT APPLICATION NUMBER: US/09/360,186  
; EARLIER FILING DATE: 1999-07-23  
; EARLIER FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 31491  
; TYPE: DNA  
; ORGANISM: Capsicum annuum  
US-09-360-186-1

Query Match 2.0%; Score 62.6; DB 3; Length 31491;  
Best Local Similarity 47.2%; Pred. No. 3.7e-07;  
Matches 265; Conservative 0; Mismatches 284; Indels 12; Gaps 2;  
QY 821 TCAAGGAGAGAGGACTTCTTGTCTAGATGATCTATGATTTTACATGATTTGGAAT 880  
Db 2234 TAAAGAGAAAGAGGACTTAAATTTCTTGGATGATATCTGGAGTTGTGAAGTGTGGGATG 2293  
QY 881 GGATAATGAAATTCATTTCTTAAGAAACAATAAGAGGCGAGTGCAGATAGTAATAACCA 940  
Db 2294 GCGTGA---GACGATGCTTTCCAACTGAAGACAATGACAGGAGTGCAGATAGTGTGACTA 2350  
QY 941 CTCGGAATGTTGATCTTGGCGAGAGTGTGCCACAGCCTCACTGGTGTACCACTTGAAT 1000

Db 2351 CCGTAAATGATGAAGTAGCTTGTATGCTGCTGTAGAGAAATTTTCTTTCGGATGAGCT 2410  
QY 1001 TCTTGCAGATGAACGATGCCATAACAATTTGCTACTGAGAAACAACAATAAATCATGAAG 1060  
Db 2411 TCATGATCAAGATGAGAGTGTGAGTCTTTTCAAAGTGCAGCAATTTTCAAGTGA----- 2465  
QY 1061 ACATGGAAATCAATTAATAATATGCAAAAGATGTTGAACGAATTTGTAATAAATGTTGTC 1120  
Db 2466 ----AGCATTAACATATGAGTTCGAGACTGTTGGAAAGCAATCGCAGATGATGTCAAG 2521  
QY 1121 GTCTACATTAAGCAATTAACAATAAGGAGTGTGCTTGCACCTAAACAGGTGTCAAGAT 1180  
Db 2522 GGTACCACCTAACTATTTGCTGTGTGAGGCTTCTCAAATCTAAAGAGCAATAGAG 2581  
QY 1181 GCGAGAAATCTATGAACACCTTCTTTCAGAACTAGAAATAAACCCAGCCTGGAAGCT 1240  
Db 2582 ATTGGAATCTGTTGCTAAAGATGTCAAGTCAATTCGTCAAAATGATCTGTGATGATCAT 2641  
QY 1241 TGAGGAGATGTTGACCTTACAGTGTCAACACCTACCATCCCATTTGAAACCATGCTTTT 1300  
Db 2642 GTTACGCTGTGCTGGGTTGAGTTAGGATCACTTGCACAGGATCTAAAGACATGCTTTC 2701  
QY 1301 TGTATCTAAGTATCTTCTTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGAT 1360  
Db 2702 TGCATTCGGAATTTTCCAGAGACAGTGAATTTCCAGTGAAGAAATTTGATGATCAT 2761  
QY 1361 GGATGACAGAGGTTTGTGTA 1381  
Db 2762 GGATGGCTGAGGGGTTCTCTGA 2782

RESULT 14  
US-09-864-680A-1  
; Sequence 1, Application US/09864680A  
; Patent No. 6762285  
; GENERAL INFORMATION:  
; APPLICANT: Staskawicz, Brian J  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Tai, Thomas H  
; TITLE OF INVENTION: B2 RESISTANCE GENE  
; FILE REFERENCE: 42250/234021 (5830-4A)  
; CURRENT APPLICATION NUMBER: US/09/864,680A  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR FILING DATE: 1999-07-23  
; PRIOR FILING DATE: 1999-07-23  
; PRIOR FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 31491  
; TYPE: DNA  
; ORGANISM: Capsicum annuum  
US-09-864-680A-1

Query Match 2.0%; Score 62.6; DB 3; Length 31491;  
Best Local Similarity 47.2%; Pred. No. 3.7e-07;  
Matches 265; Conservative 0; Mismatches 284; Indels 12; Gaps 2;  
QY 821 TCAAGGAGAGAGGACTTCTTGTCTAGATGATCTATGATTTTACATGATTTGGAAT 880  
Db 2234 TAAAGAGAAAGAGGACTTAAATTTCTTGGATGATATCTGGAGTTGTGAAGTGTGGGATG 2293  
QY 881 GGATAATGAAATTCATTTCTTAAGAAACAATAAGAGGCGAGTGCAGATAGTAATAACCA 940  
Db 2294 GCGTGA---GACGATGCTTTCCAACTGAAGACAATGACAGGAGTGCAGATAGTGTGACTA 2350  
QY 941 CTCGGAATGTTGATCTTGGCGAGAGTGTGCCACAGCCTCACTGGTGTACCACTTGAAT 1000  
Db 2351 CCGTAAATGATGAAGTAGCTTGTATGCTGTGTAGAGAAATTTTCTTTCGGATGAGCT 2410  
QY 1001 TCTTGCAGATGAACGATGCCATAACAATTTGCTACTGAGAAACAACAATAAATCATGAAG 1060

Db 2411 TCATGGATCAAGATGAGAGTGGAGTCTTTTCAAAAGTCAGCATTTTCAAGTGA----- 2465  
Qy 1061 ACATGGAATCAAAATATAATATGCAAAAGATGGTTGACGAATGTAAATAAATGTGGTC 1120  
Db 2466 -----AGCATTAACATATGATGTCGACACTGTTGGAAAGCAATCCGAGATGATGTCAGC 2521  
Qy 1121 GTCTACCATTAAGCAATTAATCAATAGGAGCTGTGCTTGGCACTTAACCAACAGGTGTCAAGAT 1180  
Db 2522 GGTATACCACTAACTATTGTGCTGTTGGAGGCTTCTCAATCTTAAAGGACCAATAGAAG 2581  
Qy 1181 GGGAGAAATCTATGAACACCTTCTTCAAGAACTAGAAATAAACCAGCCTGGAAGCTT 1240  
Db 2582 ATTGGAATACTGTTGCTTAAAGATGTCAGTCACTTCTGTCACAAATGATCCTGATGAACGAT 2641  
Qy 1241 TGAGGAGAAATGGTGACCTAGGTATCAACACCACTACCATCCATTTGAAACCAATGCTTTT 1300  
Db 2642 GTTCAGTGTGCTTGGGTTGAGTTACGATCACTTGACAAGCGATCTTAAACCAATGCTTTC 2701  
Qy 1301 TGTATCTAAGTATCTTCTCGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGAT 1360  
Db 2702 TGCATTTGGGAATTTTTCAGAAAGACAGTGATATTCAGTGAAGAAATTCATGATCAT 2761  
Qy 1361 GGATAGCAGAAGGGTTTGTGA 1381  
Db 2762 GGATGGCTGAGGGTTCCTGA 2782

## RESULT 15

US-08-947-823-2  
; Sequence 2, Application US/08947823  
; Patent No. 6114605  
; GENERAL INFORMATION:  
; APPLICANT: Williamson, Valerie M.  
; APPLICANT: Kaloshian, Isgouhi  
; APPLICANT: Yaghoobi, Jafar  
; APPLICANT: Bodeau, John  
; APPLICANT: Milligan, Stephen  
; TITLE OF INVENTION: Procedures and Materials for Conferring  
; TITLE OF INVENTION: Pest Resistance in Plants  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/947,823  
; FILING DATE: 09-OCT-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/18802  
; FILING DATE: 09-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/028,191  
; FILING DATE: 10-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-070210US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3997 base pairs  
; TYPE: nucleic acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cdna  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 85..3852  
; OTHER INFORMATION: /note= "Copy 1 cdna for M1 nematode  
; resistance gene of tomato"  
; US-08-947-823-2

Query Match 1.9%; Score 57.4; DB 3; Length 3997;  
Best Local Similarity 51.4%; Pred. No. 3.2e-06;  
Matches 161; Conservative 0; Mismatches 146; Indels 6; Gaps 1;

Qy 1241 TGAGGAGAAATGGTGACCTAGGTATCAACACCACTACCATCCCATTTGAAACCAATGCTTTT 1300  
Db 2342 TGATGAAAGTTATAGAATTAAGTTATGACCAATTTACCACATCACCTCAAGCCATGCTTC 2401  
Qy 1301 TGTATCTAAGTATCTTCTCGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGAT 1360  
Db 2402 TGTATTTTCCAAGTTTTCGAAAGGACACTTTCATTGACATCTATGAGTTGAATGTTATT 2461  
Qy 1361 GGATAGCAGAAGGGTTTGTATAGACCAAGGTTGGGATGACGACTAAGGATGTCGGAGAAA 1420  
Db 2462 TCGGTGCTGAAGGATTTGTGGGAAAGACGAGATGAACAGTATGGAAGAAAGTGTGGAAGA 2521  
Qy 1421 GTTACTTTAATGAGCTAATCAACCGAAGTATGTTCAACGATCAAGAGTGGGCATAGCAG 1480  
Db 2522 TTTATATGATGATTTAATTTTACAGTAGCTTGGTAATTTGTTTCATAG-----ATAG 2575  
Qy 1481 GAAAAATTAAGACTTTGTGCAATTCATGATATCATCCGTGATATCACAGTTTCAATCTCGA 1540  
Db 2576 GTTATGCACTGAATTTCCAAATTCATGATCTTGTGCATGACTTTTGTTCGATAAAGCAA 2635  
Qy 1541 GACAGGAAAAATTT 1553  
Db 2636 GAAAGGAAAAATTT 2648

Search completed: March 10, 2006, 00:23:52  
Job time : 535 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 21:27:02 ; Search time 2376 Seconds  
(without alignments)  
10785.691 Million cell updates/sec

Title: US-10-656-394A-7  
Perfect score: 3099  
Sequence: 1 atggcggagacgtgctgag.....gcacagctcaagctggctga 3099

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main.\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3099	100.0	3099	8	US-10-656-394A-7
2	2951.6	95.2	99090	8	US-10-656-394A-13
3	2916.2	94.1	3096	6	US-10-352-179-88
4	2910.2	93.9	3099	8	US-10-656-394A-3
5	2910.2	93.9	3674	8	US-10-656-394A-16
6	2850.2	92.0	3276	6	US-10-352-179-92
7	2820.4	91.0	76272	6	US-10-352-179-83
8	2865.2	82.8	4596	7	US-10-437-963-37316
9	2393.6	77.2	2597	7	US-10-656-394A-11
10	1882	60.7	2982	7	US-10-437-963-2483
11	1621	52.3	2422	6	US-10-656-394A-15
12	1574.2	50.8	3220	6	US-10-352-179-90
13	1562.2	50.4	2940	6	US-10-352-179-84
14	1557	50.2	2925	7	US-10-437-963-41016
15	1553.4	50.1	2982	8	US-10-656-394A-1
16	1170.6	37.8	3024	7	US-10-437-963-7778
17	1143.2	36.9	3492	7	US-10-437-963-49433
18	1133.8	36.6	2982	6	US-10-352-179-86
19	1040.4	33.6	4147	8	US-10-656-394A-5
20	1036.8	33.5	2711	7	US-10-437-963-38603
21	918.8	29.6	2365	6	US-10-352-179-96
22	838.2	27.0	2351	6	US-10-352-179-97
23	546.2	17.6	1355	6	US-10-352-179-94

24	521.8	16.8	2439	7	US-10-437-963-74853	Sequence 74853, A
25	440.8	14.2	2781	7	US-10-437-963-69440	Sequence 69440, A
26	413	13.3	1214	8	US-10-656-394A-14	Sequence 14, Appl
27	381.8	12.3	1389	8	US-10-656-394A-9	Sequence 9, Appl
28	213.4	6.9	569	7	US-10-767-701-21019	Sequence 21019, A
29	198	6.4	4026	7	US-10-437-963-32604	Sequence 32604, A
30	186.6	6.0	2931	7	US-10-437-963-70256	Sequence 70256, A
31	184	5.9	2862	3	US-09-384-453-35	Sequence 35, Appl
32	184	5.9	2862	5	US-10-267-718-35	Sequence 55316, A
33	178.6	5.8	4542	7	US-10-437-963-55316	Sequence 34, Appl
34	176.8	5.7	2954	3	US-09-354-453-34	Sequence 34, Appl
35	176.8	5.7	2954	5	US-10-267-718-34	Sequence 33, Appl
36	176.8	5.7	6760	3	US-09-354-453-33	Sequence 33, Appl
37	176.8	5.7	6760	5	US-10-267-718-33	Sequence 48577, A
38	172.6	5.6	2373	7	US-10-437-963-48577	Sequence 78921, A
39	172.6	5.6	3012	7	US-10-437-963-78921	Sequence 75977, A
40	171	5.5	2883	7	US-10-437-963-75977	Sequence 31426, A
41	165.8	5.4	3165	7	US-10-425-114-31426	Sequence 34053, A
42	165.8	5.4	3430	8	US-10-425-115-34053	Sequence 16135, A
43	165.6	5.3	2022	7	US-10-437-963-16135	Sequence 51200, A
44	165	5.3	2886	7	US-10-437-963-51200	Sequence 98981, A
45	162	5.2	2981	7	US-10-437-963-98981	

## ALIGNMENTS

RESULT 1  
US-10-656-394A-7  
; Sequence 7, Application US/10656394A  
; Publication NO. US20040210957A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang et al.  
; TITLE OF INVENTION: Cloning and Characterization of the  
; FILE REFERENCE: 035718/252062  
; CURRENT APPLICATION NUMBER: US/10/656,394A  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 3099  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(3099)  
US-10-656-394A-7

Query Match	100.0%	Score 3099;	DB 8;	Length 3099;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3099;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
Qy	1	ATGGCGGAGACGGTGTGCTGAGCATGGCAGGTGCTGTGGGCGAGCGCCATCAGCAAGGCC	60	
Db	1	ATGGCGGAGACGGTGTGCTGAGCATGGCAGGTGCTGTGGGCGAGCGCCATCAGCAAGGCC	60	
Qy	61	GCCTCGCTGCTGCCGACGACGACGCTCTCTCTGCGCGCTCGAGAAAGACATCTGGTAT	120	
Db	61	GCCTCGCTGCTGCCGACGACGACGCTCTCTCTGCGCGCTCGAGAAAGACATCTGGTAT	120	
Qy	121	ATCAAAGATGAGCTAAAAACGATCAAGCAATTCCTTAGAGCTGCTGAACCTTATGAAAAAG	180	
Db	121	ATCAAAGATGAGCTAAAAACGATCAAGCAATTCCTTAGAGCTGCTGAACCTTATGAAAAAG	180	
Qy	181	AAAGATGAGCTATTAAGCTTTGGGCGAGCAATAGCTGACCTGTCATATGACATTGAA	240	
Db	181	AAAGATGAGCTATTAAGCTTTGGGCGAGCAATAGCTGACCTGTCATATGACATTGAA	240	
Qy	241	GATTCCTTGTGATTAAGCTTCAATATGAAAGCAAAACCTTATTCGTCAATGTTGGTG	300	
Db	241	GATTCCTTGTGATTAAGCTTCAATATGAAAGCAAAACCTTATTCGTCAATGTTGGTG	300	







Db 2461 ATGCTAACTGGAATGAGCAGCTCACTCACTGGAAGAGATCTACTATTGAGGAGCAAA 2520  
Qy 2521 CTAAGGAGAGTAAACCAATGCTGATCTTGGGCACTGCGCAACCTCATGTCTCTTCAT 2580  
Db 2521 CTAAGGAGAGTAAACCAATGCTGATCTTGGGCACTGCGCAACCTCATGTCTCTTCAT 2580  
Qy 2581 CTTTATCGGAATGCTTTCCTTGGGAGAGAGCTAGTATTTCAAAAACAGAGAGATTTCCCAAT 2640  
Db 2581 CTTTATCGGAATGCTTTCCTTGGGAGAGAGCTAGTATTTCAAAAACAGAGAGATTTCCCAAT 2640  
Qy 2641 CTTAGAACACTTTTGATTTATGAATTTGGATCAGCTTAAGAGAGATCAGATTTGAGGACGGC 2700  
Db 2641 CTTAGAACACTTTTGATTTATGAATTTGGATCAGCTTAAGAGAGATCAGATTTGAGGACGGC 2700  
Qy 2701 AGCTCACCCCTTTTGGAAAAAGATAGAAATAGGCGAGTGCGAGTTGGAAATCTGGGATTACT 2760  
Db 2701 AGCTCACCCCTTTTGGAAAAAGATAGAAATAGGCGAGTGCGAGTTGGAAATCTGGGATTACT 2760  
Qy 2761 GGTATCATTCACCTTCCAAAGCTCAAGGAGATTCCTAATTAGATACGGAAGTAAAGTGGCT 2820  
Db 2761 GGTATCATTCACCTTCCAAAGCTCAAGGAGATTCCTAATTAGATACGGAAGTAAAGTGGCT 2820  
Qy 2821 GGGCTTGGTCACTCGAGGAGAGAGTGAACGCAACCCAAATCGCCCGTGTCTTAATG 2880  
Db 2821 GGGCTTGGTCACTCGAGGAGAGAGTGAACGCAACCCAAATCGCCCGTGTCTTAATG 2880  
Qy 2881 TACAGTGACCGAGAGATTCAGACCTGGGGCTGAGCGGAGGATCTTCTATAGAGTG 2940  
Db 2881 TACAGTGACCGAGAGATTCAGACCTGGGGCTGAGCGGAGGATCTTCTATAGAGTG 2940  
Qy 2941 CAAACAGCAGATCTCTTCTGATGCCGAGGATCAGTCACTGTAGCAGTGAAGCAAG 3000  
Db 2941 CAAACAGCAGATCTCTTCTGATGCCGAGGATCAGTCACTGTAGCAGTGAAGCAAG 3000  
Qy 3001 GATCCCTTCCGAGCAGGAGAGAGCTGCGAGTGCAGTGCAGTGCAGTGCAGG 3060  
Db 3001 GATCCCTTCCGAGCAGGAGAGAGCTGCGAGTGCAGTGCAGTGCAGTGCAGG 3060  
Qy 3061 AATGATAGCGAAGAGATAGGCACAGCTCAAGCTGGCTGA 3099  
Db 3061 AATGATAGCGAAGAGATAGGCACAGCTCAAGCTGGCTGA 3099

## RESULT 2

US-10-656-394A-13  
; Sequence 13, Application US/10656394A  
; Publication No. US20040210957A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang et al.  
; TITLE OF INVENTION: Cloning and Characterization of the  
; FILE OF INVENTION: Broad-spectrum resistance gene P12  
; FILE REFERENCE: 035718/252062  
; CURRENT APPLICATION NUMBER: US/10/656.394A  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 99090  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 23216  
; OTHER INFORMATION: n = A,T,C or G  
US-10-656-394A-13

Query Match 95.2%; Score 2951.6; DB 8; Length 99090;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2954; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 116 GGTATATCAAGATGAGCTTAAACGATGCAAGCAATTCCTTAGAGCTGCTGAATTCGA 175  
Db 77633 GGTATATCAAGATGAGCTTAAACGATGCAAGCAATTCCTTAGAGCTGCTGAATTCGA 77692

Qy 176 AAAAGAAAGATGAACCTATTAAAGTTGGGAGAGCAAAATACTGACCTGTCTATGACA 235  
Db 77693 AAAAGAAAGATGAACCTATTAAAGTTGGGAGAGCAAAATACTGACCTGTCTATGACA 77752  
Qy 236 TTGAAGATTCCTCTTGGTGAATTTAAAGTCCATATTCGAAGCCAAACCCCTATTTCGTCACT 295  
Db 77753 TTGAAGATTCCTCTTGGTGAATTTAAAGTCCATATTCGAAGCCAAACCCCTATTTCGTCACT 77812  
Qy 296 TGGTGAACACTCAGAGAACGCGACCGAATTCCTATCCGTATCCAAACCTTTAAATCAAGAG 355  
Db 77813 TGGTGAACACTCAGAGAACGCGACCGAATTCCTATCCGTATCCAAACCTTTAAATCAAGAG 77872  
Qy 356 TTGAAGAGTCAAGTACGAGGAAACACAGCTTACAGTTTGTAGTCAAGCCCTATTTCCTCTGGCA 415  
Db 77873 TTGAAGAGTCAAGTACGAGGAAACACAGCTTACAGTTTGTAGTCAAGCCCTATTTCCTCTGGCA 77932  
Qy 416 CAGAGATTGACATGGATTTCCTATTCGAGAGACATTCGTAAATCAGTCAAGTTCGCAATGTGG 475  
Db 77933 CAGAGATTGACATGGATTTCCTATTCGAGAGACATTCGTAAATCAGTCAAGTTCGCAATGTGG 77992  
Qy 476 ATGAGCTGAGCTTGTGGGTTTCTGACCTCCAGAGAAAGGCTGTGAAATGATCGATA 535  
Db 77993 ATGAGCTGAGCTTGTGGGTTTCTGACCTCCAGAGAAAGGCTGTGAAATGATCGATA 78052  
Qy 536 CCAATGCTAAATGATGGTCCGCGCAAGGTAATCTGTGTGTGGGATGGGTGGTTAGGCA 595  
Db 78053 CCAATGCTAAATGATGGTCCGCGCAAGGTAATCTGTGTGTGGGATGGGTGGTTAGGCA 78112  
Qy 596 AGACAGCTTTCGAGGAGATCTTTGAAAGCGAAGAGACATTTAGGAAGAACTTCCCTT 655  
Db 78113 AGACAGCTTTCGAGGAGATCTTTGAAAGCGAAGAGACATTTAGGAAGAACTTCCCTT 78172  
Qy 656 GCAATGCTTGGATTACAGTGTCACAATTCATTTCAAGGATGAGTCACTTAAAGATATGA 715  
Db 78173 GCAATGCTTGGATTACAGTGTCACAATTCATTTCAAGGATGAGTCACTTAAAGATATGA 78232  
Qy 716 TAGGCCAATCTTGGGCGCCAGTCTCTGATCAACTTGCAGAAATTTGCAAGGGAAGG 775  
Db 78233 TAGGCCAATCTTGGGCGCCAGTCTCTGATCAACTTGCAGAAATTTGCAAGGGAAGG 78292  
Qy 776 TGGTGTGCAAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGT 835  
Db 78293 TGGTGTGCAAGTACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGT 78352  
Qy 836 ACTTTGTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGATTAATGAAATG 895  
Db 78353 ACTTTGTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGATTAATGAAATG 78412  
Qy 896 CATTTCTTAAGAAACAAATAAGAGGCGAGTCCGAATAGTAATAACCACTCCGGAATGTTGATC 955  
Db 78413 CATTTCTTAAGAAACAAATAAGAGGCGAGTCCGAATAGTAATAACCACTCCGGAATGTTGATC 78472  
Qy 956 TTGCGGAGAGTGTGCGACAGCTCCTGTTGTACCACTTGTGATTTCTTTCGAGAGTGAAG 1015  
Db 78473 TTGCGGAGAGTGTGCGACAGCTCCTGTTGTGATCACTTGTGATTTCTTTCGAGAGTGAAG 78532  
Qy 1016 ATGCCATAACATTTGCTACTGAGAAAAACAAATAAATCATAGAGACATGGAATCAATA 1075  
Db 78533 ATGCCATAACATTTGCTACTGAGAAAAACAAATAAATCATAGAGACATGGAATCAATA 78592  
Qy 1076 AAAATATGCAAAAGATGTTGAACGAATTTGTAATAATGTTGCTCTACCTACCTATGCAA 1135  
Db 78593 AAAATATGCAAAAGATGTTGAACGAATTTGTAATAATGTTGCTCTACCTACCTATGCAA 78652  
Qy 1136 TACTTTACAAATAGGAGTGTCTTCCAACTAAACAGGTTGTCAGAAATGCGAGAAATTTCTATG 1195  
Db 78653 TACTTTACAAATAGGAGTGTCTTCCAACTAAACAGGTTGTCAGAAATGCGAGAAATTTCTATG 78712  
Qy 1196 AACACCTTCTTTCAGAACTAGAAATAAACCCAGCTGGAAGCTTTTGAAGAGAGATGCTGA 1255  
Db 78713 AACACCTTCTTTCAGAACTAGAAATAAACCCAGCTGGAAGCTTTTGAAGAGAGATGCTGA 78772

Qy	1256	CCCTAGGTTACACCACTACATCCATTTGGAACCAATGCTTTTGTATCTAGTATCT	1315
Db	78773	CCCTAGGTTACACCACTACATCCATTTGGAACCAATGCTTTTGTATCTAGTATCT	78832
Qy	1316	TTCTCGAGGATTTTGAATCAAAAGGAAATCGTCTAGTAGGTAGATGATAGCAAGGCT	1375
Db	78833	TTCTCGAGGATTTTGAATCAAAAGGAAATCGTCTAGTAGGTAGATGATAGCAAGGCT	78892
Qy	1376	TTGTTTAGACCAAAAGTTGGGATGCAAGCTTAAGGATGTCGGAGAGTTACTTTAATGAGC	1435
Db	78893	TTGTTTAGACCAAAAGTTGGGATGCAAGCTTAAGGATGTCGGAGAGTTACTTTAATGAGC	78952
Qy	1436	TAATCAACCGGAAGTATGATTTCAACGATCAAGAGTGGGCATAGCAGGAAAAAATTAAGACTT	1495
Db	78953	TAATCAACCGGAAGTATGATTTCAACGATCAAGAGTGGGCATAGCAGGAAAAAATTAAGACTT	79012
Qy	1496	GTGCGAATTCATGATATCATCCGTTGATATCACAGTTTCAATCTCGAGCAGGAAAAATTTTG	1555
Db	79013	GTGCGAATTCATGATATCATCCGTTGATATCACAGTTTCAATCTCGAGCAGGAAAAATTTTG	79072
Qy	1556	TATTAATACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAAAAACATCGCCACATAGCAT	1615
Db	79073	TATTAATACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAAAAACATCGCCACATAGCAT	79132
Qy	1616	TCCATGGGAGTATGTCCTGCAAAACCTGGATTTGGATTTGGAGCATTTTCGATCATTAGCTA	1675
Db	79133	TCCATGGGAGTATGTCCTGCAAAACCTGGATTTGGATTTGGAGCATTTTCGATCATTAGCTA	79192
Qy	1676	TTTTTGTGTGACAGACCAAGAGCTTAGCAATGCAATGTCAGATTCATTTGAGGATGT	1735
Db	79193	TTTTTGTGTGACAGACCAAGAGCTTAGCAATGCAATGTCAGATTCATTTGAGGATGT	79252
Qy	1736	TACGGGCTCTCGATCTTTGAGATGTGACATTCCTTAATCACTCAAAAAGATTTTCGACCGTA	1795
Db	79253	TACGGGCTCTCGATCTTTGAGATGTGACATTCCTTAATCACTCAAAAAGATTTTCGACCGTA	79312
Qy	1796	TTGCATTTGTGCGCACTTGAAATACCTTGAGTATTTGGATTTGTGCATCCATATATTCAC	1855
Db	79313	TTGCATTTGTGCGCACTTGAAATACCTTGAGTATTTGGATTTGTGCATCCATATATTCAC	79372
Qy	1856	TTCCAGAGTCAATTTGTTAAACTACAGGGCTACAAACTTTGAAACATGCCGAGCACATACA	1915
Db	79373	TTCCAGAGTCAATTTGTTAAACTACAGGGCTACAAACTTTGAAACATGCCGAGCACATACA	79432
Qy	1916	TTGCAGCACTACCAAGTGAGATCAGTAAATCTCCAATGTCGCTGATPACTCTTGTGTGTATAG	1975
Db	79433	TTGCAGCACTACCAAGTGAGATCAGTAAATCTCCAATGTCGCTGATPACTCTTGTGTGTATAG	79492
Qy	1976	GACAGTTTCATTATGACAACTTTTAGTCTAAACCCCAATGAGTGCATAACTTAAACAA	2035
Db	79493	GACAGTTTCATTATGACAACTTTTAGTCTAAACCCCAATGAGTGCATAACTTAAACAA	79552
Qy	2036	TATGCTGCCTTAAAGTATTACAACCTTTAGTTAGTTCGCGATGATCGTGCAGAAACAAATTG	2095
Db	79553	TATGCTGCCTTAAAGTATTACAACCTTTAGTTAGTTCGCGATGATCGTGCAGAAACAAATTG	79612
Qy	2096	CTGAATTGCAATGCGCCACAAAGTTGCTGCTCTGAATCAATCGGTGTGAAGGTACCCA	2155
Db	79613	CTGAATTGCAATGCGCCACCAANAGTTGCTGCTCTGAATCAATCGGTGTGAAGGTACCCA	79672
Qy	2156	AAGGNAATAGTTAGTTTCGAGACTTCGAGTCTTAGAGTATGTAGATATTCAGCGGACCA	2215
Db	79673	AAGGNAATAGTTAGTTTCGAGACTTCGAGTCTTAGAGTATGTAGATATTCAGCGGACCA	79732
Qy	2216	GTATAGTAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAGGNAATTAGGTGTGACAA	2275
Db	79733	GTATAGTAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAGGNAATTAGGTGTGACAA	79792
Qy	2276	CAACCGGTTCGACAAAGGAAAAATGTAGATCTTTATGAGCCATTTGAGAGCTCTCTT	2335
Db	79793	CAACCGGTTCGACAAAGGAAAAATGTAGATCTTTATGAGCCATTTGAGAGCTCTCTT	79852
Qy	2336	CCCTCCAACTCTCTCCATGTGATGCTGCAAGGAATCTCAGATGTGGGAACATTTGAGTGCC	2395

Db	79853	CCCTCCAAATCTTCCAATGTGATGCTGCAGGAATCTCAGATGGTGGAAACATTTGAGTGCC	79912
Qy	2396	TAGATTCTATTTCAATCTCTCTCTCCCTACTGAGGACACTCGTGTGGATGGAAATCTTTG	2455
Db	79913	TAGATTCTATTTCAATCTCTCTCTCCCTACTGAGGACACTCGTGTGGATGGAAATCTTTG	79972
Qy	2456	AGGAGATGCTCACTACTCGATTGAGCAGCTCACCTGAAGAAGATCTACTTTATTGAGGA	2515
Db	79973	AGGAGATGCTCACTACTCGATTGAGCAGCTCACCTGAGAGAGATCTACTTTATTGAGGA	80032
Qy	2516	GCAAACTAAAGGAAGGTAAAAACATGCTGATACTTTGGGGCACTGCCAAACCTCATGTGTC	2575
Db	80033	GCAAACTAAAGGAAGGTAAAAACATGCTGATACTTTGGGGCACTGCCAAACCTCATGTGTC	80092
Qy	2576	TTCAATCTTTATCGGAATGCTTACCTTTGGGCGAAGCTAGTATTTCAAAAACAGGAGCATTC	2635
Db	80093	TTCAATCTTTATCGGAATGCTTACCTTTGGGCGAAGCTAGTATTTCAAAAACAGGAGCATTC	80152
Qy	2636	CAAACTCTTAGAACACATTTGGATTTATGAATTCGATCAGCTAAGAGAGATCAGATTTGAGG	2695
Db	80153	CAAACTCTTAGAACACATTTGGATTTATGAATTCGATCAGCTAAGAGAGATCAGATTTGAGG	80212
Qy	2696	ACGGCAGCTCACCCCTGTTTGGAAAAAGATAGAAATAGGCGAGTGCGCAGGTTTGGAAATCTGGGA	2755
Db	80213	ACGGCAGCTCACCCCTGTTTGGAAAAAGATAGAAATAGGCGAGTGCGCAGGTTTGGAAATCTGGGA	80272
Qy	2756	TTACTGGTATCATTTACCTTCCAAAGCTCAAGGAGATTCCAATTAGATACGGAGTAAG	2815
Db	80273	TTACTGGTATCATTTACCTTCCAAAGCTCAAGGAGATTCCAATTAGATACGGAGTAAG	80332
Qy	2816	TGCTCGGGCTTGCTCAGCTGGAGGGAGAGTGAAACGACACCCAAATCGCCCCGTCGTC	2875
Db	80333	TGCTCGGGCTTGCTCAGCTGGAGGGAGAGTGAAACGACACCCAAATCGCCCCGTCGTC	80392
Qy	2876	TAATGTACAGTGACCGAAGGTATCAGACTGGGGGCTGAGCCGAGAGATCTCTATAG	2935
Db	80393	TAATGTACAGTGACCGAAGGTATCAGACTGGGGGCTGAGCCGAGAGATCTCTCTATAG	80452
Qy	2936	AAGTGAACACAGCAGATCCTGTTCTGTATGCCGAAGGATCAGTCACTGTAGCAGTGGAA	2995
Db	80453	AAGTGAACACAGCAGATCCTGTTCTGTATGCCGAAGGATCAGTCACTGTAGCAGTGGAA	80512
Qy	2996	CAACGATCCCTTCCGACGAGGAGGAGAGCTCCGAGTCCGAGGTGATCAGTTGA	3055
Db	80513	CAACGATCCCTTCCGACGAGGAGGAGAGCTCCGAGTCCGAGGTGATCAGTTGA	80572
Qy	3056	CGACGAATGATACGGAAG	3073
Db	80573	CGACGAATGATAGTCTCAG	80590

```

RESULT 3
US-10-352-179-88
; Sequence 88, Application US/10352179
; Publication No. US20040006788A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Guo-liang
; APPLICANT: Liu, Guifu
; TITLE OF INVENTION: Procedures and Materi-
; FILE REFERENCE: 2727/04108
; CURRENT APPLICATION NUMBER: US/10/352,179
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: 60/352,106
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 88
; LENGTH: 3096
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS

```

LOCATION: (1)..(3096)  
OTHER INFORMATION:  
US-10-352-179-88

Query Match									
Best Local Similarity 94.1%; Score 2916.2; DB 6; Length 3096;									
Matches 2975; Conservative 0; Mismatches 98; Indels 0; Gaps 0;									
Qy	1	ATGCGGAGACGGTGTCTGAGCATGGCGAGGTCGTGGTGGGCGACGCCATCAGCAAGGCC	60						
Db	1	ATGCGGAGACGGTGTCTGAGCATGGCGAGGTCGTGGTGGGCGACGCCATCAGCAAGGCC	60						
Qy	61	GCCTCGCTGCTGCCGAGACGACGACGCTGCTGGCTGGCGTGGGAGAACACATCTGGTAT	120						
Db	61	GCCTCGCTGCTGCCGAGACGACGACGCTGCTGGCTGGCGTGGGAGAACACATCTGGTAT	120						
Qy	121	ATCAAGATGAGCTATCAAAACGATGCAAGCATCTCTTAGAGCTGCTGAACCTTATGAAAAAG	180						
Db	121	ATCAAGATGAGCTATCAAAACGATGCAAGCATCTCTTAGAGCTGCTGAACCTTATGAAAAAG	180						
Qy	181	AAAGATGAATCTATTAAGGTTTGGCGAGACGAAATACGTGACCTGTCTATGACATGAA	240						
Db	181	AAAGATGAATCTATTAAGGTTTGGCGAGACGAAATACGTGACCTGTCTATGACATGAA	240						
Qy	241	GATTCCCTTGTGATGAATTTAAGGTCCATATGAAAGCCAAACCCCTATTTCTCAGTTGGTG	300						
Db	241	GATTCCCTTGTGATGAATTTAAGGTCCATATGAAAGCCAAACCCCTATTTCTCAGTTGGTG	300						
Qy	301	AAACTCAGAGAACGCCACGCAATTCGTATCCGTATCCACAACTTAAATCAAGAGTTGAA	360						
Db	301	AAACTCAGAGAACGCCACGCAATTCGTATCCGTATCCACAACTTAAATCAAGAGTTGAA	360						
Qy	361	GAAGTCAAGTAGCAGGAAACACACGCTACAGTTTGTAGTCAAGCTATTTCTCTGCGACAGAG	420						
Db	361	GAAGTCAAGTAGCAGGAAACACACGCTACAGTTTGTAGTCAAGCTATTTCTCTGCGACAGAG	420						
Qy	421	ATTGAATGGAATTCCTATGAGAGACATTCGTATATCATGCTCAGCTGCAATGGATGAG	480						
Db	421	GATGACATGGAATTCCTATGAGAGACATTCGTATATCATGCTCAGCTGCAATGGATGAA	480						
Qy	481	GCTGAGCTTGTGGGTTTCTGACTCCAAAGAAAGGCTGCTTGAATGATCGATACCAAT	540						
Db	481	GCTGAGCTTGTGGGTTTCTGACTCCAAAGAAAGGCTGCTTGAATGATCGATACCAAT	540						
Qy	541	GCTAATGATGGTCCGCGCAAGGTAATCTGTGTGTGGGATGGGTGTGGTGGCAAGACA	600						
Db	541	GCTAATGATGGTCCGCGCAAGGTAATCTGTGTGTGGGATGGGTGTGGTGGCAAGACA	600						
Qy	601	GCTCTTTCGAGGAGATCTTTCGAAAGCGAAGACATGAGGAAAGAACTTCCCTGCAAT	660						
Db	601	GCTCTTTCGAGGAGATCTTTCGAAAGCGAAGACATGAGGAAAGAACTTCCCTGCAAT	660						
Qy	661	GCTTGGATTACAGTGTCAATCTTTCAGAGATGAGCTACTTAAAGATATGATACGC	720						
Db	661	GCTTGGATTACAGTGTCAATCTTTCAGAGATGAGCTACTTAAAGATATGATACGC	720						
Qy	721	CAACTTCTGGGCGGAGTCTCTGGATCAATCTTTCGAGAAATTTGCAAGGGAAGGTGGT	780						
Db	721	CAACTTCTGGGCGGAGTCTCTGGATCAATCTTTCGAGAAATTTGCAAGGGAAGGTGGT	780						
Qy	781	GTGCAAGTACATCATCTTCTGAGTACCTGTAGAGAGCTCAAGGAGAAAGAGGTACTTT	840						
Db	781	GTGCAAGTACATCATCTTCTGAGTACCTGTAGAGAGCTCAAGGAGAAAGAGGTACTTT	840						
Qy	841	GTGTTCTAGATGATCTATGGAATTTTACATGATGGAATTTGATTAATGAAATGCAATTT	900						
Db	841	GTGTTCTAGATGATCTATGGAATTTTACATGATGGAATTTGATTAATGAAATGCAATTT	900						
Qy	901	CCTAAGAACAAATGAAGAGGCGAGTGGATAGTAAATCAACCTCGGAATGTGTGCGG	960						
Db	901	CCTAAGAACAAATGAAGAGGCGAGTGGATAGTAAATCAACCTCGGAATGTGTGCGG	960						
Qy	961	GAGAGTGTGCCACAGCCTCACTGGTGTACCACTTGTATTTCTTTCAGATGACGATGCC	1020						

Db	961	GAGAGTGTGCCACAGCCTCACTGGTGTACACCTTGTATTTCTTTCAGATGACGATGCC	1020						
Qy	1021	ATAACATTGCTACTGAGAAAAACAAATAAAATCATGAAGACATGGAATCAAAATAAAAT	1080						
Db	1021	ATAACATTGCTACTGAGAAAAACAAATAAAATCATGAAGACATGGAATCAAAATAAAAT	1080						
Qy	1081	ATGCAAAAGATGGTTGAACGAATTTAAATAAATGTTGCTCTACCATTAGCAATCTT	1140						
Db	1081	ATGCAAAAGATGGTTGAACGAATTTAAATAAATGTTGCTCTACCATTAGCAATCTT	1140						
Qy	1141	ACAAATAGGAGCTGTCTTGCACAACTAAACAGGTGTGAGAAATGGAAGAAATCTATGAACAC	1200						
Db	1141	ACAAATAGGAGCTGTCTTGCACAACTAAACAGGTGTGAGAAATGGAAGAAATCTATGAACAC	1200						
Qy	1201	CTTCTTTCAGAACTAGAAATTAACCCAGGCTTGGAGCTTTGAGGAGAAATGGTGACCTTA	1260						
Db	1201	CTTCTTTCAGAACTAGAAATTAACCCAGGCTTGGAGCTTTGAGGAGAAATGGTGACCTTA	1260						
Qy	1261	GGTTACAAACCACTACCATCCATTTGAAACCACTGCTTTTGTATCTAAGTATCTTTCTCT	1320						
Db	1261	GGTTACAAACCACTACCATCCATCTGAAACCACTGCTTTTGTATCTAAGTATCTTTCTCT	1320						
Qy	1321	GAGGATTTTGAATCAAAAGGAATCTGCTAGTAGGTAGATGAGTAGCAGAGGGTTGTT	1380						
Db	1321	GAGGATTTTGAATCAAAAGGAATCTGCTAGTAGGTAGATGAGTAGCAGAGGGTTGTT	1380						
Qy	1381	AGACCAAAAGGTTGGGATGACGACTTAAGATCTCGGAGAAATTTAATGAGCTAAATC	1440						
Db	1381	AGACCAAAAGGTTGGGATGACGACTTAAGATCTCGGAGAAATTTAATGAGCTAAATC	1440						
Qy	1441	AACCGAAGTATGATTCACAGATCAAGAGTGGGCAATAGCAGAGAAATTAAGACTTGTGCA	1500						
Db	1441	AACCGAAGTATGATTCACAGATCAAGAGTGGGCAATAGCAGAGAAATTAAGACTTGTGCA	1500						
Qy	1501	ATTCTATGATATCATCCGCTGATATCAAGTTTCAATCTCGAGACAGGAAATTTGTATTA	1560						
Db	1501	ATTCTATGATATCATCCGCTGATATCAAGTTTCAATCTCGAGACAGGAAATTTGTATTA	1560						
Qy	1561	TTACCAATGGGAGATGGCTCTGATTTAGTTTCCGAGAAACA CTGCGCACATAGCAATCCAT	1620						
Db	1561	TTACCAATGGGAGATGGCTCTGATTTAGTTTCCGAGAAACA CTGCGCACATAGCAATCCAT	1620						
Qy	1621	GGGATGATGCTCTGCAAACTGGATTTGATTTGAGCAATTTATTCATTTAGCTATTTT	1680						
Db	1621	GGGATGATGCTCTGCAAACTGGATTTGATTTGAGCAATTTATTCATTTAGCTATTTT	1680						
Qy	1681	GGTGAAGACCCCAAGATCTAGCACTGCAAGTTTGTCCAGATCAATTTGAGGATGTTACGG	1740						
Db	1681	GGTGAAGACCCCAAGATCTAGCACTGCAAGTTTGTCCAGATCAATTTGAGGATGTTACGG	1740						
Qy	1741	GTCTTGGATCTTGAAGATGTCACATTTCTTAATCACTCAAAAGATTTCCGACCGTATTGCA	1800						
Db	1741	GTCTTGGATCTTGAAGATGTCACATTTCTTAATCACTCAAAAGATTTCCGACCGTATTGCA	1800						
Qy	1801	TTGTTGTGCACTTCAAAATCTTGAATTTGGAATTTCTCATCCATATATTCATTTCCC	1860						
Db	1801	TTGTTGTGCACTTCAAAATCTTGAATTTGGAATTTCTCATCCATATATTCATTTCCC	1860						
Qy	1861	AGATCCATTTGTAACCTACAGGCTTCAAACTTTTGAACATGCGGACATACATTTGCA	1920						
Db	1861	AGATCCATTTGTAACCTACAGGCTTCAAACTTTTGAACATGCGGACATACATTTGCA	1920						
Qy	1921	GCACTACCAAGTGAGATCAGTAAACTCTCAATGTCTGATATCTCTTGTGTATGAGACAG	1980						
Db	1921	GCACTACCAAGTGAGATCAGTAAACTCTCAATGTCTGATATCTCTTGTGTATGAGACAG	1980						
Qy	1981	TTTCTATTGACAACTTTAGTCTAAACCCCAATGAGGTGATTAACCAATATTC	2040						
Db	1981	TTTCTATTGACAACTTTAGTCTAAACCCCAATGAGGTGATTAACCAATATTC	2040						
Qy	2041	CTGCTTAAAGTATTCACACCTTTTAGTTAGTCCGATGATCTGTCMAAACAAATTTGCTGAA	2100						

```

Db 2041 CTGCCTAAAGTATTACACCTTTAGTTCGCGATGATCGTGCACAAACAAATTCCTGAA 2100
Qy 2101 TTGCACATGGCCACCAAAAGTTGCTGCTGCTGATCAATCGGTGTGAAGGTACCAAGGA 2160
Db 2101 TTGCACATGGCCACCAAAAGTTGCTGCTGCTGATCAATCGGTGTGAAGGTACCAAGGA 2160
Qy 2161 ATAGGTAAAGTTGCGAGACTTGCAGGTTCTAGAGTATGTAGATATCAGGCGGACCAAGT 2220
Db 2161 ATAGGTAAAGTTGCGAGACTTGCAGGTTCTAGAGTATGTAGATATCAGGCGGACCAAGT 2220
Qy 2221 AGAGCAATCAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAATTTAGGTGTGACACAAAC 2280
Db 2221 AGAGCAATCAAGAGCTGGGCGACTTAAAGCAAGTTGAGGAATTTAGGTGTGATAACAAA 2280
Qy 2281 GGGTCGCAAAAGGAAATTTAAGATACCTTTATGAGGCACTTGAAGAGCTCTCTCCCTC 2340
Db 2281 GGGTCGCAAAAGGAAATTTAAGATACCTTTATGAGGCACTTGAAGAGCTCTCTCCCTC 2340
Qy 2341 CAATCTCTCAATGTGAGTGTGAGGAATCTCAGATGTGGAACACATTTAGTGTGCTAGAT 2400
Db 2341 CAATCTCTCAATGTGAGTGTGAGGAATTTATCAGATATTTGAACACATTTAGTGTGCTAGAT 2400
Qy 2401 TCTATTTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
Db 2401 TCTATTTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
Qy 2461 ATGCTTAATCGGATTCAGAGCTCTACTACCTGGAAGAGATCTACTTTATTTAGAGGACAA 2520
Db 2461 ATGCTTAATCGGATTCAGAGCTCTACTACCTGGAAGAGATCTACTTTATTTAGAGGACAA 2520
Qy 2521 CTAAGGAGGATTAACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2580
Db 2521 CTAAGGAGGATTAACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2580
Qy 2581 CTTTATCGGAATCTTACTCTGCGGAGAGCTAGTATTTCAAAAAGAGAGATTTCCCAAT 2640
Db 2581 CTTTATCGGAATCTTACTCTGCGGAGAGCTAGTATTTCAAAAAGAGAGATTTCCCAAT 2640
Qy 2641 CTTAGACACTTTGGATTTATGAATTTGATCAGCTAAGAGAGATCAGATTTGAGGAGCGC 2700
Db 2641 CTTAGACACTTTGGATTTATGAATTTGATCAGCTAAGAGAGATCAGATTTGAGGAGCGC 2700
Qy 2701 AGCTACCCCTGTTGGAAGAGATGAGAAATGAGCGAGTGCAGGTTGGAATCTGGAATFAC 2760
Db 2701 AGCTACCCCTGTTGGAAGAGATGAGAAATCTCTGCTGAGGTTGGAATCAGGATFAT 2760
Qy 2761 GGTATCACTTCACTTCCAAAGCTCAGGAGATTTCCAAATTTAGATACGGAAGTAAAGTGGCT 2820
Db 2761 GGTATCACTTCACTTCCAAAGCTCAGGAGATTTCCAAATTTAGATACGGAAGTAAAGTGGCT 2820
Qy 2821 GGGTTTGGTTCAGTGTGAGGAGAGTGAACGACACCAATTCGCCCCGCTGCTGCTAATG 2880
Db 2821 AGGCTTGGTTCAGTGTGAGGAGAGTGAACACACCAATTCGCCCCGCTGCTGCTAATG 2880
Qy 2881 TACAGTACCGAAGGATATCAGACCTGCGGCTGAAGCGGAGAGATCTTCTATAGAAGTG 2940
Db 2881 GACAGTACCGAAGGATATCAGACCTGCGGCTGAAGCGGAGAGATCTTCTATAGAAGTG 2940
Qy 2941 CAAACAGCAGATCTGTCTCTGATGCGGAGGATCAGTCACTGATGAGTGAAGCAAGC 3000
Db 2941 CAAACAGCAGATCTGTCTCTGATGCGGAGGATCAGTCACTGATGAGTGAAGCAAGC 3000
Qy 3001 GATCCCTTCCGAGGAGGAGAGAGCTCGCAGTGCAGGTTGATCAGTTCGAGCAGC 3060
Db 3001 GATCCCTTCCGAGGAGGAGAGAGCTCGCAGTGCAGGTTGATCAGTTCGAGCAGC 3060
Qy 3061 AATGATAGCGAAG 3073
Db 3061 AATGATAGCGAAG 3073
Qy 3073
Db 3073

```

```

; Sequence 3, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3099)
US-10-656-394A-3

```

```

Query Match 93.9%; Score 2910.2; DB 8; Length 3099;
Best Local Similarity 96.2%; Pred. No. 0;
Matches 2981; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

```

```

Qy 1 ATGGCGGAGACGCTGCTGAGCATGCGGAGTGCCTGCTGGGCGAGCGGCATCAGCAAGGCC 60
Db 1 ATGGCGGAGACGCTGCTGAGCATGCGGAGTGCCTGCTGGGCGAGCGGCATCAGCAAGGCC 60
Qy 61 GCCTCCGCTGTCGCGAGAGACCAAGCTCTCTGCTGGGCGTTCGAGAAAGACATCTGGTAT 120
Db 61 GCCTCCGCTGTCGCGAGAGACCAAGCTCTCTGCTGGGCGTTCGAGAAAGACATCTGGTAT 120
Qy 121 ATCAAGATGAGCTAAAGCAATGCAAGCATTCCTTAGAGCTGCTGAACCTTATGAAAAAG 180
Db 121 ATCAAGATGAGCTAAAGCAATGCAAGCATTCCTTAGAGCTGCTGAAGCTTATGAAAAAG 180
Qy 181 AAAGATGAATCTATTAAAGTTTGGCGAGAGCAAAATACGTGACCTGTCTATGACATTGAA 240
Db 181 AAAGATGAATCTATTAAAGTTTGGCGAGAGCAAAATACGTGACCTGTCTATGACATTGAA 240
Qy 241 GATTCCTCTGATGAATTTAAAGTCCATATCAAGGCGCAAAACCTTATTCGTCAAGTTGGTG 300
Db 241 GATTCCTCTGATGAATTTAAAGTCCATATGAGGCGCAAAACCTTATTCGTCAAGTTGGTG 300
Qy 301 AAATCTCAGAGAACGCCACCGAATTCCTATCCGTATCCAACTTCAACCTTAAATCAAGATTGAA 360
Db 301 AAATCTCAGAGAACGCCACCGAATTCCTATCCGTATCCAACTTCAACCTTAAATCAAGATTGAA 360
Qy 361 GAAGTCAGTAGCAGGAGACACACGCTACAGTTTATGTCAGGCTATTTCTCTGCGCACAGAG 420
Db 361 GAAGTCAGTAGCAGGAGACACACGCTACAGTTTATGTCAGGCTATTTCTCTGCGCACAGAG 420
Qy 421 ATTGACATCGATTCCTATGCGAGAGACATTCGTAAATCAGTCAGCTCGCAATTTGGATGAG 480
Db 421 ATTGACATCGATTCCTATGCGAGAGACATTCGTAAATCAGTCAGCTCGCAATTTGGATGAG 480
Qy 481 GCTGAGCTTGTGGGTTTTCTGACCTCAAGAAAGAGGCTGTTGAAATGATCGATACCAAT 540
Db 481 GCTGAGCTTGTGGGTTTTCTGACCTCAAGAAAGAGGCTGTTGAAATGATCGATACCAAT 540
Qy 541 GCTAAATGATGGTCCGCGCAAGGTAAATCTGTGTTGTTGGGATGGGTGTTAGGCAAGACA 600
Db 541 GCTAAATGATGGTCCGCGCAAGGTAAATCTGTGTTGTTGGGATGGGTGTTAGGCAAGACA 600
Qy 601 GCTCTTTCGAGGAGATCTTTGAAGCGAGAGACATTAGGAGAGACTTCCCTTGCAT 660
Db 601 GCTCTTTCGAGGAGATCTTTGAAGCGAGAGACATTAGGAGAGACTTCCCTTGCAT 660
Qy 661 GCTTGGATTAAGTGTCAAAATCATTTTCAAGGATGAGCTACTTAAAGATATGATACGC 720
Db 661 GCTTGGATTAAGTGTCAAAATCATTTTCAAGGATGAGCTACTTAAAGATATGATACGC 720
Qy 721 CAACCTTCTTGGCCCCCAGTCTCTGATCACTCTTGCAGAAATTTGCAAGGAGGAGTGGTG 780

```

Db 721 CAACCTCTTGGTCCAGTTCTCTGGATCAACTCTTGGATGAATTCGAAGGAAGTGGTG 780  
Qy 781 GTGCAAGTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGTACTTT 840  
Db 781 GTGCAAGTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGGTACTTT 840  
Qy 841 GTTGTCTTAGATCATCTAGGATTTTACATGATGGAAATGGATPAATGAATGGCAATTT 900  
Db 841 GTTGTCTTAGATCATCTAGGATTTTACATGATGGAAATGGATPAATGAATGGCAATTT 900  
Qy 901 CTTAAGAACATAGAGAGGAGCTCGAATAGTAATTAACCACTCGGAATGTTGATCTGGG 960  
Db 901 CTTAAGAACATAGAGAGGAGCTCGAATAGTAATTAACCACTCGGAATGTTGATCTGGG 960  
Qy 961 GAGAAGTGTGCCACAGCTCACTGGTGTACCACTTGTATTTCTTTCAGATGAACGATGCC 1020  
Db 961 GAGAAGTGTGCCACAGCTCACTGGTGTACCACTTGTATTTCTTTCAGATGAACGATGCC 1020  
Qy 1021 ATAACTATGCTACTGAGAAACAAATAAATCATGAGAGATGAATCAATTAATAT 1080  
Db 1021 ATTTCAATGCTACTGAGAAACAAATAAATCATGAGAGATGAATCAATTAATAT 1080  
Qy 1081 ATGCAAAAGATGTTGAAAGCAATTTGAAATAAATGCTGCTGCTACCAATAGCAATCTT 1140  
Db 1081 ATGCAAAAGATGTTGAAAGCAATTTGAAATAAATGCTGCTGCTACCAATAGCAATCTT 1140  
Qy 1141 ACAATAGAGCTGCTGCTGCAACTAAACAGGTGTCAGATGGAGAAATTTCTATGAACAC 1200  
Db 1141 ACAATAGAGCTGCTGCTGCAACTAAACAGGTGTCAGATGGAGAAATTTCTATGAACAA 1200  
Qy 1201 CTTCTCTCAGAACTAGAAATTAACCAAGCTGAGAGCTTTGAGAGAGATGGTGAACCTA 1260  
Db 1201 CTTCTCTCAGAACTAGAAATTAACCAAGCTGAGAGCTTTGAGAGAGATGGTGAACCTA 1260  
Qy 1261 GGTTCACCAACCTACATCCCATTTGAAACCAATGCTTTTGTATCTTAAGTATCTTTCCT 1320  
Db 1261 GGTTCACCAACCTACATCCCATTTGAAACCAATGCTTTTGTATCTTAAGTATCTTTCCT 1320  
Qy 1321 GAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTACATGATAGAGAGAGGTGTTGT 1380  
Db 1321 GAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTACATGATAGAGAGAGGTGTTGT 1380  
Qy 1381 AGACCAAGTGTGGATGACGACTAAGAGTGTGGAGAAAGTTACTTTAATGAGCTAATC 1440  
Db 1381 AGACCAAGTGTGGATGACGACTAAGAGTGTGGAGAAAGTTACTTTAATGAGCTAATC 1440  
Qy 1441 AACCGAGTATGATTCACAGATCAAGAGTGGGATAGCAGGAAATTAAGACTTGTGGA 1500  
Db 1441 AACCGAGTATGATTCACAGATCAAGAGTGGGATAGCAGGAAATTAAGACTTGTGGA 1500  
Qy 1501 ATTCAATGATATCACTCGTATATCAAGTTTCAATCTCGAGACAGGAAATTTGTGATTA 1560  
Db 1501 ATTCAATGATATCACTCGTATATCAAGTTTCAATCTCGAGACAGGAAATTTGTGATTA 1560  
Qy 1561 TTACCAATGGAGATGGCTGCTGATTTAGTTCAGGAAACACTCCGACATAGCATTTCCAT 1620  
Db 1561 TTACCAATGGAGATGGCTGCTGATTTAGTTCAGGAAACACTCCGACATAGCATTTCCAT 1620  
Qy 1621 GGGAGTATGTCCTGCAAAACAGGATTTGATTTGAGATTCATTTGATGATTTT 1680  
Db 1621 GGGAGTATGTCCTGCAAAACAGGATTTGATTTGAGATTCATTTGATGATTTT 1680  
Qy 1681 GGTGACAGACCCAGAGTCTAGCAGATGAGTTGTCAGATCAATTTGAGATGTTACGG 1740  
Db 1681 GGTGACAGACCCAGAGTCTAGCAGATGAGTTGTCAGATCAATTTGAGATGTTACGG 1740  
Qy 1741 GTCTTGGATCTTGAAGATGACATTTCTTAATCACTCAAAAGATTTGACCGGATTTGCA 1800  
Db 1741 GTCTTGGATCTTGAAGATGACATTTCTTAATCACTCAAAAGATTTGACCGGATTTGCA 1800  
Qy 1801 TTGTTGTGCCACTTGAATATCTGAGTATTTGATTTGATTTGATTTGATTTGATTTGATTT 1860

Db 1801 TTGTTGTGCCACTTGAATATCTGAGTATTTGATTTGATTTGATTTGATTTGATTTGATTT 1860  
Qy 1861 AGATCATTTGGTAAACTACAGGGCTTACAAACTTTGAACTGCGGACACATACATTGCA 1920  
Db 1861 AGATCATTTGGTAAACTACAGGGCTTACAGAGCTTTGAACTGCGGACACATACATTGCA 1920  
Qy 1921 GCATACCAAGTGAATCAGTAACTCAATGCTGCTGATCTCTTCTGTTATAGGACAG 1980  
Db 1921 GCATACCAAGTGAATCAGTAACTCAATGCTGCTGATCTCTTCTGTTATAGGAGAG 1980  
Qy 1981 TTTTATTTATGACAACTTTAGTCTAAACCAACCACTGAAAGTGCATTAACACAAATATGC 2040  
Db 1981 TTTTATTTATGACAACTTTAGTCTAAACCAACCACTGAAAGTGCATTAACACAAATATGC 2040  
Qy 2041 CTGCTTAAAGTATTTACACCTTTAGTTCGATGATGCTGCAAAACAAATTTGCTGAA 2100  
Db 2041 CTGCTTAAAGTATTTACACCTTTAGTTCGATGATGCTGCAAAACAAATTTGCTGAA 2100  
Qy 2101 TTGCACATGGCCACCAAAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
Db 2101 TTGCACATGGCCACCAAAAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
Qy 2161 ATAGGTAAAGTTCGAGACTTTGAGGTTCTAGAGTATGATGATATCAGGCGGACAGTAGT 2220  
Db 2161 ATAGGTAAAGTTCGAGACTTTGAGGTTCTAGAGTATGATGATATCAGGCGGACAGTAGT 2220  
Qy 2221 AGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAAATTTAGGTGTGACAAAC 2280  
Db 2221 AGAGCAATCAAAAGAGCTGGGCGAGTTAAGCAAGCTGAGGAAATTTAGGTGTGACAAAC 2280  
Qy 2281 GGTTCGACAAAGGAAATTTAAGATATCTTTATGAGCAGCATTTGAGAGTCTCTTCTCCTC 2340  
Db 2281 GGTTCGACAAAGGAAATTTAAGATATCTTTATGAGCAGCATTTGAGAGTCTCTTCTCCTC 2340  
Qy 2341 CAATCTCTCAATGCTGAGTGTGAGGAAATCTCAGATGCTGAGGAAACACTTTGAGTGTCTAGAT 2400  
Db 2341 CAATCTCTCAATGCTGAGTGTGAGGAAATCTCAGATGCTGAGGAAACACTTTGAGTGTCTAGAT 2400  
Qy 2401 TCTATTTCT 2460  
Db 2401 TCTATTTCT 2460  
Qy 2461 ATGCTTAACTGGATTTGAGCAGCTCACTCACTGAGGAGATCTACTTATTTGAGGAGCAAA 2520  
Db 2461 ATGCTTAACTGGATTTGAGCAGCTCACTCACTGAGGAGATCTACTTATTTGAGGAGTAAA 2520  
Qy 2521 CTAAGGAAAGTAAACCAATGCTGATCTTGGGCACTGCGCAACCTCATGTTCTCTTCTCT 2580  
Db 2521 CTAAGGAAAGTAAACCAATGCTGATCTTGGGCACTGCGCAACCTCATGTTCTCTTCTCT 2580  
Qy 2581 CTTTATCGGATGCTTACTCTTGGGAGAGCTAGTATTTCAAAACAGGAGCATTTCCCAAT 2640  
Db 2581 CTTTATCGGATGCTTACTCTTGGGAGAGCTAGTATTTCAAAACAGGAGCATTTCCCAAT 2640  
Qy 2641 CTTAGAACACTTTGATTTTGAATTTGATCAGCTAAGAGAGATCAGATTTGAGGAGCGC 2700  
Db 2641 CTTAGAACACTTTGATTTTGAATTTGATCAGCTAAGAGAGATCAGATTTGAGGAGCGC 2700  
Qy 2701 AGCTCAGCTCTGTTGGGAAAGATAGAAATAGCGGAGTGCAGGTTGGAATCTGGGATTTACT 2760  
Db 2701 AGCTCAGCTCTGTTGGGAAAGATAGAAATCTCTTGTGCGAGTTGGAATCAGGATTTACT 2760  
Qy 2761 GGTATCATTTCACTTCCCAAGCTCAAGGAGATTTCAATTTAGATACGGAAGTGAAGTGGCT 2820  
Db 2761 GGTATCATTTCACTTCCCAAGCTCAAGGAGATTTCAATTTAGATACGGAAGTGAAGTGGCT 2820  
Qy 2821 GGGCTTTGGTCACTGAGGAGAGTGAACGACACCCCAATCCGCGCTGCTGCTAATG 2880  
Db 2821 GGGCTTTGGTCACTGAGGAGAGTGAACGACACCCCAATCCGCGCTGCTGCTAATG 2880  
Qy 2881 TACAGTGAACGAGAGTATCAACCTCTGGGGGCTGAAGCCGAGGATCTTTCTATAGAGATG 2940  
Db 2881 TACAGTGAACGAGAGTATCAACCTCTGGGGGCTGAAGCCGAGGATCTTTCTATAGAGATG 2940



QY	2941	CAAA	CAGCAGATCCTGTTCTGTATGCCGAGGATCAGTCACTGTAGCAGTGGAGCAACG	3000
Db	2941	CAAA	CAGCAGATCCTGTTCTGTATGCCGAGGATCAGTCACTGTAGCAGTGGAGCAACG	3000
QY	3001	GATCCCTTCCGAGCAGGAGGAGAGCTCGCAGTCCGAGTGTCATCAGTTGACGACG	3060	
Db	3001	GATCCCTTCCGAGCAGGAGGAGAGCTCGCAGTCCGAGTGTCATCAGTTGACGACG	3060	
QY	3061	AATGATCGGAAGATAGGCACAGCTCAAGCTGGGCTGA	3099	
Db	3061	AATGATCGGAAGATAGGCACAGCTCAAGCTGGGCTGA	3099	

## RESULT 5

US-10-656-394A-16

03-10-038-394A-10  
: Sequence 16. Application US/10656394A

Publication No. US20040210957A1

: PUBLICATION NO: 0320

APPLICANT: Wang et al.

APPLICANT: wang et al.  
: TITLE OF INVENTION: Cloning and Characterization of the

;  
: TITLE OF INVENTION: CROUING AND CHARACTERIZATION OF THE  
: TITLE OF INVENTION: broad-spectrum resistance gene *Pi2*

FILE REFERENCE: 035718/252062

FILE REFERENCE: 035/16/232062  
CURRENT APPLICATION NUMBER: US/19

;; CURRENT APPLICATION NUMBER  
: CURRENT FILING DATE. 200

; CURRENT FILING DATE: 2003-09-05  
 ; NUMBER OF SEQ TO NOS: 16

; NUMBER OF SE  
: SOFTWARE: FA; SOFTWARE: FASO  
: SEQ ID NO 16

```

; SEQ ID NO 1
:      LENGTH: 36

```

LENGTH: 3674  
TYPE: DNA

TYPE: DNA  
ORGANISM: Oryz

Query Match 93.9%; Score 2910.2; DB 8; Length 3674;  
Best Local Similarity 96.2%; Pred. No. 0;  
Matches 2981; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY	1	ATGCGGAGAGCGGTGCTTGACATGCGCGAGGTGCGCTCGTGGCAGCGCCCATCAGCAAGGCC	60
Db	9	ATGCGGAGAGCGGTGCTGAGCATGCGAGGTGCGCTCGTGGCAGGTGCCATCAGCAGGCC	68
QY	61	GCCTCGCGTGTGCGCAGCAGACGAGCCTCCTCTCGTGGCGTGCAGAAAGACATCTGGTAT	120
Db	69	GCCTCTGCGCGTCCCAATGAGACGAGCGCTCTCTCGTGGCGTGCAGAAAGACATCTGGTAT	128
QY	121	ATCAAGATGAGCTTAAAAAGATCGATCGACGATTCCTTAGAGCTGCTGAACCTTATGAAAG	180
Db	129	ATCAAGATGAGCTTAAAAAGCAATCAGGCAATTCCTTAGAGCTGCTGAAGTATGAAAG	188
QY	181	AAAGATGAACATTATAAGGTTTGGCGCAGAGCAAAATACGTGACCTGTCTCATATGACATTGAA	240
Db	189	AAAGATGAACATTATAAGGTTTGGCGCAGAGCAAAATACGTGACCTGTCTGATGACATTGAA	248
QY	241	GATTCCTTGATGAATTTAAGTCCATATTGAAAGCAAAACCTATTTCGTCACTGGTG	300
Db	249	GATTCCTTGATGAATTTAAAGTCCATATTGAAAGCAAAACCTATTTCGTCACTGGTG	308
QY	301	AAACTCAGAGAAACGCGACCGAATTCCTACCGTATCCACAACCTTAAATCAAGAGTTGAA	360
Db	309	AACTTAGNAGCGGCCACCGATCGCTATCCGTATCCACAACTCAATCAAGAGTTGAA	368
QY	361	GAAGTGAGTAGCAGGAACAACGCTACAGTTTATGTAAGCCTATTTCCTTGGCACAGAG	420
Db	369	GAAGTGAGTAGCAGGAACAACGCTACAAATTTAGTCGAGCCTATTTCCTCCGGCACAGAG	428
QY	421	ATTGACATCGAATTCCTATGCAAGAGACATTCGTAATCAGTTCAGCTCGCAATGTGATCGAG	480
Db	429	GATGACATCGAATTCCTATGCAAGAGACATTCGCATCAATCAGCTCGAAATGTGGATGAA	488
QY	481	GCTGAGCTGTGGGTTTTCTTGACTCCAGAAAAGGCTGCTGGAATGATGATCAATCCAAAT	540
Db	489	GCTGAGCTGTGGGTTTTCTTGACTCCAGAAAAGGCTGCTGGAATGATGATCAATCCAAAT	548

Db 1629 GCGAGTATGTCCTGCAAAACAGGATGGATTGGAGCAATATTCGATCAITAGCTATTTT 1688  
Qy 1681 GGTGACGACCCCAAGAGTCTAGCACATCGAGTTTGTCCAGATCAATTTGAGGATGTTACGG 1740  
Db 1689 GGTGACGACCCCAAGAGTCTAGCACATCGAGTTTGTCCAGATCAATTTGAGGATGTTACGG 1748  
Qy 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCTCAAAAGAGTTTCGACCGATGCA 1800  
Db 1749 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCTCAAAAGAGTTTCGACCGATGCA 1808  
Qy 1801 TTGCTTGCCACTTGAATTAATCTTGAATTTGAGTATCGATATTCGATCAATTTGATTTCC 1860  
Db 1809 TTGCTTGCCACTTGAATTAATCTTGAATTTGAGTATTCGATATTCGATCAATTTGATTTCC 1868  
Qy 1861 AGATCAATTTGTAATCTAGGGCTTACAACTTTTGAACATGCGGACGACATACATGCA 1920  
Db 1869 AGATCAATTTGTAATCTAGGGCTTACAGACTTTTGAACATGTCAGGACATACATGCA 1928  
Qy 1921 GCACTACCAAGTGAATCAGTAACTCCAAATGTCGATCTCTGTTGTATGAGACG 1980  
Db 1929 GCACTACCAAGTGAATCAGTAACTCCAAATGTCGATCTCTGTTGTATGAGACG 1988  
Qy 1981 TTTCAATATGACAACTTTAGTCTAAACCAACCAATGAAGTGCATTAACATATATGC 2040  
Db 1989 CTTGAATTTGACAACTTTAGTCTAAATCAACCAATGAAGTGCATTAACATATATGC 2048  
Qy 2041 CTGCTTAAAGTATTCACACTTTAGTCTGCGATGATCGTCGAAACCAATTTGCTGAA 2100  
Db 2049 CTGCTTAAAGTATTCACACTTTAGTCTGCGATGATCGTCGAAACCAATTTGCTGAA 2108  
Qy 2101 TTGCACATGGCCACCAAAAGTTTCTGGTCTGAATCAATCGTGTGAAGGTACCCAAAGCA 2160  
Db 2109 TTTCAATGGCCACCAAAAGTTTCTGGTCTGAATCAATCGTGTGAAGGTACCCAAAGCA 2168  
Qy 2161 ATAGTAAAGTGGGAGCTTGCAGTTCTAGAGTATGTAGATATCAGGCGGACAGTAGT 2220  
Db 2169 ATAGTAAAGTGGGAGCTTGCAGTTCTAGAGTATGTAGATATCAGGCGGACAGTAGT 2228  
Qy 2221 AGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGCTGAGGAAATTTAGTGTGACAAACAAAC 2280  
Db 2229 AGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGTTAGGAAATTTAGTGTGACAAACAAAC 2288  
Qy 2281 GGTGCGACAAAGAAATGTAAGATATCTTATGAGCCATTTGAGAGCTCTCTTCCCTC 2340  
Db 2289 GGTGCGACAAAGAAATGTAAGATATCTTATGAGCCATTTGAGAGCTCTCTTCCCTC 2348  
Qy 2341 CAATCTCTCATGTGATGCTGACGAAATCTCAGATGTTGAAACACTTGAAGTCCCTAGAT 2400  
Db 2349 CAATCTCTCATGTGATGCTGCTGTTATATCAGATTTGAACACTTGAAGTCCCTAGAT 2408  
Qy 2401 TCTATTTCAATCT 2460  
Db 2409 TCTATTTCAATCT 2468  
Qy 2461 ATGCTTAACTGAGTGAAGAGCTCACTCACTGAGGAGGATCTACTTATTTGAGAGCAAA 2520  
Db 2469 ATGCTTAACTGAGTGAAGAGCTCACTCACTGAGGAGGATCTACTTATTTGAGAGTAAA 2528  
Qy 2521 CTAAGGAAAGGTAACCAATGCTGATATCTGGGCACTGGCCCACTCATGTCCTTTCAT 2580  
Db 2529 CTAAGGAAAGGTAACCAATGCTGATATCTGGGCACTGGCCCACTCATGTCCTTTCAT 2588  
Qy 2581 CTTTATCGGAATGCTTACTTGGGAGAGAGCTAGTATTTCAAAACAGGAGCATTTCCCAAT 2640  
Db 2589 CTTTATCATATTTCTTATCTTGGGAGAGAGCTAGTATTTCAAAACAGGAGCATTTCCCAAT 2648  
Qy 2641 CTTAGAACACTTTGGAATTTAATTTGATCAGCTAAAGAGATCAAGTTTGGAGCGGC 2700  
Db 2649 CTTAGAACACTTTGGAATTTAATTTGATCAGCTAAAGAGATCAAGTTTGGAGCGGC 2708  
Qy 2701 AGCTCACCCCTGTTGGAAGATAGAAATAGCGAGTGGAGTTGGAATCTGGGATCTACT 2760

Db 2709 AGCTCACCCCTGTTGGAAGATAGAAATCTTGTGCGAGGTTGGAATCAGGATTTAT 2768  
Qy 2761 GGTATCATTTCACTTCCAAAGCTCAAGGAGATTTCCAAATAGATACGGAAGTAAAGTGGCT 2820  
Db 2769 GGTATCATTTCACTTCCAAAGCTCAAGGAGATTTCACTTGAATACAAAGTAAAGTGGCT 2828  
Qy 2821 GGGCTTGTGCTAGCTGAGGAGGAGAGTGAACGACACCCAAATCCGCCCTGCTGCTAATG 2880  
Db 2829 AGGCTTGTGCTAGCTGAGGAGGAGAGTGAACACACCCAAATCCGCCCTGCTGCGAATG 2888  
Qy 2881 TACAGTGAACCAAGATATCACGACTCGGGGCTGGAAGCCGAAGGATCTCTATAGAATG 2940  
Db 2889 GACAGTGAACCAAGGATATCACGACTCGGGGCTGGAAGCCGAAGGATCTCTATAGAATG 2948  
Qy 2941 CAAAACAGAGATCTCTGTTCTGATGCGGAAGGATCAGTCACTGTAGCAGTGGAGCAAG 3000  
Db 2949 CAAAACAGAGATCTCTGTTCTGATGCGGAAGGATCAGTCACTGTAGCAGTGGAGCAAG 3008  
Qy 3001 GATCCCTTCCGAGCAGGAGGAGAGCTCGCAGTCCGAGGTGATCACGTTGACGAG 3060  
Db 3009 GATCCCTTCCGAGCAGGAGGAGAGCTCGCAGTCCGAGGTGATCACGTTGACGAG 3068  
Qy 3061 AATGATAGCAAGAGATAGGACACAGCTCAAGCTGGCTGA 3099  
Db 3069 AATGATAGCAAGAGATAGGACACAGCTCAAGCTGGCTGA 3107

## RESULT 6

US-10-352-179-92  
; Sequence 92, Application US/10352179  
; Publication No. US20040006788A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Guo-liang  
; APPLICANT: Liu, Guifu  
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in P  
; FILE REFERENCE: 22727/04108  
; CURRENT APPLICATION NUMBER: US/10/352,179  
; PRIOR FILING DATE: 2003-01-27  
; PRIOR APPLICATION NUMBER: 60/352,106  
; PRIOR FILING DATE: 2002-01-25  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 92  
; LENGTH: 3276  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3276)  
; OTHER INFORMATION:  
US-10-352-179-92

Query Match 92.0%; Score 2850.2; DB 6; Length 3276;  
Best Local Similarity 97.2%; Pred. No. 0;  
Matches 2900; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 117 GTATATCAAGATGAGCTTAAAGAGTGAAGGATGCAAGCAATTCCTTAGAGCTGCTGAATATGAA 176  
Db 294 GTATATCAAGATGAGCTTAAAGAGTGAAGGATGCAAGCAATTCCTTAGAGCTGCTGAATATGAA 353  
Qy 177 AAAGAAAGATGAATATTTAAAGGTTTGGGAGAGCAAAATACGTAACCTGTCTATATGACAT 236  
Db 354 AAAGAAAGATGAATATTTAAAGGTTTGGGAGAGCAAAATACGTAACCTGTCTATATGACAT 413  
Qy 237 TCAAGATTCCTTGAATGAATTTAAGGTCCTATTTGAAAGCCAAACCTATTTTCGTCAGTT 296  
Db 414 TGAAGATTCCTTGAATGAATTTAAGGTCCTATTTGAAAGCCAAACCTATTTTCGTCAGTT 473  
Qy 297 GGTGAAATCTAGAGAAACCGCAACCGAATGCTATTCGATATCCCAACCTTAAATCAAGAGT 356  
Db 474 GGTGAAATCTAGAGAAACCGCAACCGAATGCTATTCGATATCCCAACCTTAAATCAAGAGT 533  
Qy 357 TGAAGAGTGAAGTGAAGGAGCAACACGCTACAGTTTGTAGTCAAGCTTATTTCTCTGGCAC 416

Db 534 TGAAGAAGTGTGATGACGAGAACACACGCTACAGTTTGTAGTCAAGGCTATTTCTCTCGGCAC 593  
Qy 417 AGAGATTGACATCGGATTCCTATGCGAGAGACATTCGTTAATCAGTCAGCTCGCAATGTGGA 476  
Db 594 AGAGATTGACATCGGATTCCTATGCGAGAGACATTCGTTAATCAGTCAGCTCGCAATGTGGA 653  
Qy 477 TGAGGCTGAGCTTGTGGGTTTTCTGACTCCAAAGAAAGGCTGCTGAAATGATCGATAC 536  
Db 654 TGAAGCTGAGCTTGTGGGTTTTCTGACTCCAAAGAAAGGTTGCTTGAAATGATCGATAC 713  
Qy 537 CAATGCTAATGATGTGTCGCGCCAGGTAATCTGTGTTGTTGGGATGGGTGGTTAGGCAA 596  
Db 714 CAATGCTAATGATGTGTCGCGCCAGGTAATCTGTGTTGTTGGGATGGGTGGTTAGGCAA 773  
Qy 597 GACAGCTCTTTCCAGGAGAGATCTTTGAAAGCGAGAGACATTAAGGAAGAACTTCCCTTG 656  
Db 774 GACAGCTCTTTCCAGGAGAGATCTTTGAAAGCGAGAGACATTAAGGAAGAACTTCCCTTG 833  
Qy 657 CAATGCTGATTAAGTGTGCAATCAATCAATTTCAAGGATGAGCTTCAAGAGATGAT 716  
Db 834 CAATGCTGATTAAGTGTGCAATCAATCAATTTCAAGGATGAGCTTCAAGAGATGAT 893  
Qy 717 ACGCCAATCTTTGGCCCAAGTTCTCTGATCAACTCTTGCAAGATTTGCAAGGAGAGGT 776  
Db 894 ACGCCAATCTTTGGCCCAAGTTCTCTGATCAACTCTTGCAAGATTTGCAAGGAGAGGT 953  
Qy 777 GGTGGTCAAGTATCATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGTTA 836  
Db 954 GGTGGTCAAGTATCATCATCTTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGTTA 1013  
Qy 837 CTTTGTTGTTCTAGATGATCTGATTTTATCATGATTTGGAATTTGGAATTTGGAATTTGGAATTTG 896  
Db 1014 CTTTGTTGTTCTAGATGATCTGATTTTATCATGATTTGGAATTTGGAATTTGGAATTTGGAATTTG 1073  
Qy 897 ATTTCTTAAGAACAAATGAAGGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATCT 956  
Db 1074 ATTTCTTAAGAACAAATGAAGGCGAGTCGAATAGTAATAACCACTCGGAATGTTGATCT 1133  
Qy 957 TGCGGAGAGTGTGCCACAGCTCTACCTGTTGACCACTTCAATTTCTGACAGATGAACGA 1016  
Db 1134 AGCGGAGAGTGTGCCACAGCTCTACCTGTTGACCACTTCAATTTCTGACAGATGAACGA 1193  
Qy 1017 TGCCATAAATCTGCTAGAGAAAACAAATATAAATCATGAGACATGGAATCAATATA 1076  
Db 1194 TGCCATAAATCTGCTAGAGAAAACAAATATAAATCATGAGACATGGAATCAATATA 1253  
Qy 1077 AATATGCAAAAGATGTTGCAAGGATTTGTAATAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1136  
Db 1254 AATATGCAAAAGATGTTGCAAGGATTTGTAATAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1313  
Qy 1137 ACTTAATAGGAGCTGTGTTGCAACTTAAACAGAGTGTGAGATGGGAGAAATTTCTATGA 1196  
Db 1314 ACTTAATAGGAGCTGTGTTGCAACTTAAACAGAGTGTGAGATGGGAGAAATTTCTATGA 1373  
Qy 1197 ACACCTTCTTGAAGTGAATAAATCCCAAGCTTGAAGCTTTGAGGAGATGTTGAC 1256  
Db 1374 ACACCTTCTTGAAGTGAATAAATCCCAAGCTTGAAGCTTTGAGGAGATGTTGAC 1433  
Qy 1257 CCTAGGTTACACCACTACCATCCCATTTGAAACCATGCTTTTGTATCTAAGTATCTT 1316  
Db 1434 CCTAGGTTACACCACTACCATCCCATTTGAAACCATGCTTTTGTATCTAAGTATCTT 1493  
Qy 1317 TCCTGAGGATTTTGAATCAAAAGGATCTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1376  
Db 1494 TCCTGAGGATTTTGAATCAAAAGGATCTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 1553  
Qy 1377 TGTTAGACCAAGGTTGGGATGACGACTAAGGATGTCGAGGAGAAAGTTTACTTTTAATGAGCT 1436  
Db 1554 TGTTAGACCAAGGTTGGGATGACGACTAAGGATGTCGAGGAGAAAGTTTACTTTTAATGAGCT 1613  
Qy 1437 AATCAACCGAGTATGATTTCAAGATCAAGAGTGGGATAGCAGGAGAAATTAAGACTTG 1496

Db 1614 AATCAGCCGAGTATGATTTCAACGATCAAGAGTGGGCATATCAGGAAAAAATTAAGACTTG 1673  
Qy 1497 TCGAATTCATGATATCATTCGTTGATATCAAGTTTCAATCTCGAGACAGGAAAAATTTTGT 1556  
Db 1674 TCGAATTCATGATATCATTCGTTGATATCAAGTTTCAATCTCGAGACAGGAAAAATTTTGT 1733  
Qy 1557 ATTATTACCAATGGGAGATGCTCTGATTAGTTTCAAGAAAAACAATCGGACACATAGCATT 1616  
Db 1734 ATTATTACCAATGGGAGATGCTCTGATTAGTTTCAAGAAAAACAATCGGACACATAGCATT 1793  
Qy 1617 CCAATGGGAGTATGCTCGAAAACTGGATTTGGATTTGGAGCATTTTTCGATCATTAGCTAT 1676  
Db 1794 CCAATGGGAGTATGCTCGAAAACTGGATTTGGATTTGGAGCATTTTTCGATCATTAGCTAT 1853  
Qy 1677 TTTTGGTGAACAGACCAAGAGCTTAGCACATGCAATTTTGTCCAGATCAATTTGAGGATGTT 1736  
Db 1854 TTTTGGTGAACAGACCAAGAGCTTAGCACATGCAATTTTGTCTAGATCAATTTGAGGATGTT 1913  
Qy 1737 ACGGCTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAAGATTTGACCGTAT 1796  
Db 1914 ACGGCTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAAAGATTTGACCGTAT 1973  
Qy 1797 TGCATTTGTTGTCACACTTTGAAATATCTTGAGTATTTGGAATTTTCGTATCCATATTTCACT 1856  
Db 1974 TGCATTTGTTGTCACACTTTGAAATATCTTGAGTATTTGGATATTTTCGTATCCATATTTCACT 2033  
Qy 1857 TCCAGATCCATTTGGTAAACTACAGGGCTTACAACTTTGAAATTTGAAATTTGAAATTTGAAATTTG 1916  
Db 2034 TCCAGATCCATTTGGTAAACTACAGGGCTTACAACTTTGAAATTTGAAATTTGAAATTTGAAATTTG 2093  
Qy 1917 TGCAGCACTACCAAGTGAAGTCAAGTAACTCCAAATGTCGCATACCTCTCTGTTGTATAGG 1976  
Db 2094 TGCAGCACTACCAAGTGAAGTCAAGTAACTCCAAATGTCGCATACCTCTCTGTTGTATAGG 2153  
Qy 1977 ACAGTTTCAATTTGACAACTTTTGTCTTAAACCCCAATGAAAGTGAATTAACCAAT 2036  
Db 2154 AAAGTTTGTATGACAACTTTTGTCTTAAACCCCAATGAAAGTGAATTAACCAAT 2213  
Qy 2037 ATGCTCTGCTTAAGTATTTACACCTTTTGTAGTTAGTTCGCGATGATCGTGCAAAACAAATTCG 2096  
Db 2214 ATGCTCTGCTTAAGTATTTACACCTTTTGTAGTTAGTTCGCGATGATCGTGCAAAACAAATTCG 2273  
Qy 2097 TGAATTTGACATGGGCCCAAAAGTTGCTGCTGATCAATCGGTGTGAGATGCCAA 2156  
Db 2274 TGAATTTGACATGGGCCCAAAAGTTGCTGCTGATCAATCGGTGTGAGATGCCAA 2333  
Qy 2157 AGGAATAGGTAAGTTTGCAGACTTTCAGAGTTTCTAGAGTATGTAGATATGTAGATATGTAGATATGTAG 2216  
Db 2334 AGGAATAGGTAAGTTTGCAGACTTTCAGAGTTTCTAGAGTATGTAGATATGTAGATATGTAGATATGTAG 2393  
Qy 2217 TAGTAGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGCTGAGGAAATTTAGTGTGACAC 2276  
Db 2394 TAGTAGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGCTTGAAGGAAATTTAGTGTGACAA 2453  
Qy 2277 AAACGGTTCGACAAAGGAAAAATGTAAAGTACTTTATGAGCCATTTGAGAGCTCTCTTC 2336  
Db 2454 AAACGGTTCGACAAAGGAAAAATGTAAAGTACTTTATGAGCCATTTGAGAGCTCTCTTC 2513  
Qy 2337 CCTCCAAATCTCTCATCT 2396  
Db 2514 CCTCCAAATCTCTCATCT 2573  
Qy 2397 AGATTTCTATTTCT 2456  
Db 2574 AGATTTCTATTTCT 2633  
Qy 2457 GGAGATGCTTAATCGGATTTGAGAGCTCACTCACTGAGGAAATCTCTATTTATTTAGGAG 2516  
Db 2634 AGAGATGCTTAATCGGATTTGAGAGCTCACTCACTGAGGAAATCTCTATTTATTTAGGAG 2693  
Qy 2517 CAACTTAAAGGAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGG 2576  
Db 2694 CAACTTAAAGGAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGG 2753



QY 2577 TCATCTTTTACGAAATGCTTACCTTGGGAGAGAGCTAGTATTCAAAAACAGGAGCAATCCC 2636  
 DB 2754 TTATCTTTTATGGAATGCTTACCTTGGGAGAGAGCTAGTATTCAAAACGGGAGCAATCCC 2813  
 QY 2637 AAATCTTGAACACTTTTGGATTTATGAATTTGATCAGCTAGAGAGAGATCAGATTTGAGA 2696  
 DB 2814 AAATCTTGAACACTTTTGGATTTATGAATTTGATCAGCTAGAGAGAGATCAGATTTGAGA 2873  
 QY 2697 CGGCAGCTCACCCCTGTTGGAAAGATAGAAATAGCGGAGTGCAGGTTCGAAATCTGGAT 2756  
 DB 2874 TGGCAGCTCACCCCTGTTGGAAAGATAGAAATCTTGGCTGCAGGTTCGAAATCTGGAT 2933  
 QY 2757 TACTGTGATCATTTCACTTCCAAAGCTCAAGGAGATTTCAATTTAGATACGGAAGTAAAGT 2816  
 DB 2934 TATTGGTATCATTTCACTTCCAAAGCTCAAGGAGATTTCACTTGAATACAAAGTAAAGT 2993  
 QY 2817 GGCTGGCTTTGGTCACTGGAGGAGAGTGAACGACACCAAAATCGCCCGTGTGCT 2876  
 DB 2994 GGCTAGCTTTGGTCACTGGAGGAGAGTGAACGACACCAAAATCGCCCGTGTGCT 3053  
 QY 2877 AATGTACAGTGAACGAGATTCACGACTGGGGGCTGAAGCCGAGAGATTTCTATAGA 2936  
 DB 3054 AATGTACAGTGAACGAGATTCACGACTGGGGGCTGAAGCCGAGAGATTTCTATAGA 3113  
 QY 2937 AGTCAACAGCAGATCTGTTCCCTGATGCCGAGGATCAGTCACTGTAGCAGTGAAGC 2996  
 DB 3114 AGTCAACAGCAGATCTGTTCCCTGATGCCGAGGATCAGTCACTGTAGCAGTGAAGC 3173  
 QY 2997 AACGGATCCCTTCCCGAGCAGGAGGAGAGCTCGCAGTCGAGGATTCAGCTGAC 3056  
 DB 3174 AACGGATCCCTTCCCGAGCAGGAGGAGAGCTCGCAGTCGAGGATTCAGCTGAC 3233  
 QY 3057 GACGAATGATAGCAGAGATAGGACACTCAAGCTGCCTGA 3099  
 DB 3234 GACGAATGATAGCAGAGATAGGACACTCAAGCTGCCTGA 3276

RESULT 7

US-10-352-179-83  
 ; Sequence 83, Application US/10352179  
 ; Publication No. US20040006788A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Guo-liang  
 ; APPLICANT: Liu, Guifu  
 ; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla  
 ; FILE REFERENCE: 22727/04108  
 ; CURRENT APPLICATION NUMBER: US/10/352,179  
 ; CURRENT FILING DATE: 2003-01-27  
 ; PRIOR APPLICATION NUMBER: 60/352,106  
 ; PRIOR FILING DATE: 2002-01-25  
 ; NUMBER OF SEQ ID NOS: 97  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 83  
 ; LENGTH: 76272  
 ; TYPE: DNA  
 ; ORGANISM: Oryza minuta  
 ; US-10-352-179-83

Query Match 91.0%; Score 2820.4; DB 6; Length 76272;  
 Best Local Similarity 97.1%; Pred. No. 0;  
 Matches 2872; Conservative 0; Mismatches 86; Indels 0; Gaps 0;  
 QY 116 GGTATATCAAGATGAGCTAAACAGTCCAGGATTCCTTAGAGCTGCTGAACCTATGA 175  
 DB 62061 GGTATATCAAGATGAGCTAAACAGTCCAGGATTCCTTAGAGCTGCTGAACCTATGA 62120  
 QY 176 AAAAGAAAGATGAACATTAAAGGTTTGGGAGAGCAATACGTCCTGTATATGACA 235  
 DB 62121 AAAAGAAAGATGAACATTAAAGGTTTGGGAGAGCAATACGTCCTGTATATGACA 62180  
 QY 236 TTGAAGATTCCTTGTGATTTAAGTCCATTTGAAGCCAAACCTTATTCGTCACT 295

DB 62181 TTGAAGATTCCTTGTGATTTAAGTCCATTTGAAGCCAAACCTTATTCGTCACT 62240  
 QY 296 TGGTGAACACTCAGAGAAACGCGACCGAATTTGCTATCCGTATCCCAACCTTAAATCAAGAG 355  
 DB 62241 TGGTGAACACTCAGAGAAACGCGACCGAATTTGCTATCCGTATCCCAACCTTAAATCAAGAG 62300  
 QY 356 TTGAAGACTGAGTACAGGAGACACAGCTACAGTTTGTAGTCAAGCCCTTATTCCTCTGGCA 415  
 DB 62301 TTGAAGACTGAGTACAGGAGACACAGCTACAGTTTGTAGTCAAGCCCTTATTCCTCTGGCA 62360  
 QY 416 CAGAGATTGACATGATTTCTTATGAGAGACATTTCTGTATCATAGTCAGCTGCGCAATGTGG 475  
 DB 62361 CAGAGATTGACATGATTTCTTATGAGAGACATTTCTGTATCATAGTCAGCTGCGCAATGTGG 62420  
 QY 476 ATGAGCTGAGCTTCTTGGGTTTCTGATCCAGAAAGCGCTGTGAATCATCATGATA 535  
 DB 62421 ATGAGCTGAGCTTCTTGGGTTTCTGATCCAGAAAGGTTGTCTGAATCATCATGATA 62480  
 QY 536 CCAATCTTAATGATGGTCCGCGCAAGGTAATCTGTGTTGGGATGGGTGGTTAGGCA 595  
 DB 62481 CCAATCTTAATGATGGTCCGCGCAAGGTAATCTGTGTTGGGATGGGTGGTTAGGCA 62540  
 QY 596 AGACAGCTCTTTTGGAGAGATCTTTGAAAGCGAGAGACATTTAGCAAGAACTTCCCTT 655  
 DB 62541 AGACAGCTCTTTTGGAGAGATCTTTGAAAGCGAGAGACATTTAGCAAGAACTTCCCTT 62600  
 QY 656 GCAATGCTTGGATTAAGTGTCAACATCATTTTCAAGGATTTGAGTCTTAAAGATATGA 715  
 DB 62601 GCAATGCTTGGATTAAGTGTCAACATCATTTTCAAGGATTTGAGTCTTAAAGATATGA 62660  
 QY 716 TAGCCAACTTCTTGGCCCCAGTCTCTGATCAACTCTTTCGAAGAAATTCGAAGGAGAG 775  
 DB 62661 TAGCCAACTTCTTGGCCCCAGTCTCTGATCAACTCTTTCGAAGAAATTCGAAGGAGAG 62720  
 QY 776 TGGTGTGCAAGTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGAGAGAGAGGT 835  
 DB 62721 TGGTGTGCAAGTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGAGAGAGAGGT 62780  
 QY 836 ACTTCTGTTCTTAGATGATCTAGATTTTACATGATTTGGAATTTGGAATTTGGAATTTG 895  
 DB 62781 ACTTCTGTTCTTAGATGATCTAGATTTTACATGATTTGGAATTTGGAATTTGGAATTTG 62840  
 QY 896 CATTTCTTGAACAAATTAAGAGGAGCTGCAATTAATTAACCACTTCCGAAATTTGATC 955  
 DB 62841 CATTTCTTGAACAAATTAAGAGGAGCTGCAATTAATTAACCACTTCCGAAATTTGATC 62900  
 QY 956 TTCCGAGAGAGTGTGCCACAGCTCACTGGTGTACCACTTGTATTTCTTCCAGATGAGC 1015  
 DB 62901 TAGCCGAGAGAGTGTGCCACAGCTCACTGGTGTACCACTTGTATTTCTTCCAGATGAGC 62960  
 QY 1016 ATGCCATACATTTGCTTACTGAGAAACAAATTAATTAATTAATTAATTAATTAATTAATTA 1075  
 DB 62961 ATGCCATACATTTGCTTACTGAGAAACAAATTAATTAATTAATTAATTAATTAATTAATTA 63020  
 QY 1076 AAAATATGCAAAAGATGTTGAAACGAATTTGTAATTAATTAATTAATTAATTAATTAATTA 1135  
 DB 63021 AAAATATGCAAAAGATGTTGAAACGAATTTGTAATTAATTAATTAATTAATTAATTAATTA 63080  
 QY 1136 TACTTCAATAGAGCTGTGCTTCAACATTAACAGGCTGCTAGATGCGAGAAATTTCTATG 1195  
 DB 63081 TACTTCAATAGAGCTGTGCTTCAACATTAACAGGCTGCTAGATGCGAGAAATTTCTATG 63140  
 QY 1196 AACACCTTCTTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTTTTCCAGAGAGATGCTGA 1255  
 DB 63141 AACACCTTCTTTCAGAACTAGAAATAAACCCAGCCTGGAAGCTTTTCCAGAGAGATGCTGA 63200  
 QY 1256 CCCTAGGTTTCAACCACTTACCCTCCATTTGAAACCATGCTTTTCTTCTATCTAGATCT 1315  
 DB 63201 CCCTAGGTTTCAACCACTTACCCTCCATTTGAAACCATGCTTTTCTTCTATCTAGATCT 63260  
 QY 1316 TTCTGAGGATTTTGAATCAAAAGGAATTCGTCTAGTAGGTAGATGATAGCAGAGAGGT 1375  
 DB 63261 TTCTGAGGATTTTGAATCAAAAGGAATTCGTCTAGTAGGTAGATGATAGCAGAGAGGT 63320

QY	1376	TTGTTAGACCAAGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTTAATGAGC	1435
DB	63321	TTGTTAGACCGCAGCGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTTAATGAGC	63380
QY	1436	TAACTCAACCGAAGTATGATTCAACGATCAAGAGTGGGCATAGCAGGAAAAAATTAAGACTT	1495
DB	63381	TAACTCAACCGAAGTATGATTCAACGATCAAGAGTGGGCATATCAGGAAAAAATTAAGACTT	63440
QY	1496	GTGCAATTCATGATATCATCCGCTGATATCAAGTTTTCAATCTCGAGACAGGAAAAATTTTG	1555
DB	63441	GTGCAATTCATGATATCATCCGCTGATATCAAGTTTTCAATCTCGAGACAGGAAAAATTTTG	63500
QY	1556	TATTTATTACCAATGGGAGATGGCTCTGATTTAGTTTACGAAAAACACTCGCCACATAGCAT	1615
DB	63501	TATTTATTACCAATGGGAGATGGCTCTGATTTAGTTTACGAAAAACACTCGCCACATAGCAT	63560
QY	1616	TCCATGGGATGATGTCCTGCAGAACTGGATTTGGATTGGAGCATTTATTCGATCATTAGCTA	1675
DB	63561	TCCATGGGATGATGTCCTGCAGAACTGGATTTGGATTGGAGCATTTATTCGATCATTAGCTA	63620
QY	1676	TTTTTGGTGAAGACCCAGAGTCTAGCACTGCAAGTTTGTCCAGATTCAAATGAGGATGT	1735
DB	63621	TTTTTGGTGAAGACCCAGAGTCTAGCACTGCAAGTTTGTCTAGATTCAAATGAGGATGT	63680
QY	1736	TACGGGCTCTTGATGCTTTGAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTA	1795
DB	63681	TACGGGCTCTTGATGCTTTGAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACCGTA	63740
QY	1796	TTGCATTTGTTGTGCACCTTGAANAATCTTGAGTATTTGGATATTTGCTCATTCATATATTCAC	1855
DB	63741	TTGCATTTGTTGTGCACCTTGAANAATCTTGAGTATTTGGATATTTGCTCATTCATATATTCAC	63800
QY	1856	TTCCAGAGTCCATTTGTTGAAACTACAGGGCTACAAACTTTGAACTATGCCGAGACATACA	1915
DB	63801	TTCCAGAGTCCATTTGTTGAAACTACAGGGCTACAAACTTTGAACTATGCCGAGACATACA	63860
QY	1916	TTGCAGCACTACGAATGAGATCAGTAACTCCAACTGCTGCATACCTTCGTTGTTATAG	1975
DB	63861	TTGCAGCACTACGAATGAGATCAGTAACTCCAACTGCTGCATACCTTCGTTGTTATAG	63920
QY	1976	GACAGTTTTCTATTATGACAACTTTAGTCTTAAACCACCCCAATGAAGTGATCAACTAACACAA	2035
DB	63921	GAAAGTTTGTGTTATGACAACTTTAGTCTTAAACCACCCCAATGAAGTGATCAACTAACACAA	63980
QY	2036	TATGCTGCTCTAAAGTATTCACACTTTTATGTTAGTTCGGATGATCGTGCAAAACAAATTTG	2095
DB	63981	TATGCTGCTCTAAAGTATTCACACTTTTATGTTAGTTCGGATGATCGTGCAAAACAAATTTG	64040
QY	2096	CTGAATTGCACTACGGCCACCAAAAGTTGCTGCTCTGAATCAATCGGTTGGAAGTACCCA	2155
DB	64041	CTGAATTGCACTACGGCCACCAAAAGTTGCTGCTCTGAATCAATCGGTTGGAAGTACCCA	64100
QY	2156	AAGGAAATAGGTTAAGTTCGGAGACTTCGAGGTTCTAGAGTATGTAGATATCAGGCGGACCA	2215
DB	64101	AAGGAAATAGGTTAAGTTCGGAGACTTCGAGGTTCTAGAGTATGTAGATATCAGGCGGACCA	64160
QY	2216	GTATGATAGCAATCAAAAGACTCGGGCATTTAAGCAAGCTGAGGAAATTAAGTTGTGACAA	2275
DB	64161	GTATGATAGCAATCAAAAGACTCGGGCATTTAAGCAAGCTGAGGAAATTAAGTTGTGATAA	64220
QY	2276	CAAAACGGGTCCGACAAAGGAAAAATGTAAAGTACTTTATGCAAGCCATTGGAAGCTCTCTT	2335
DB	64221	CAAAAGGCTCGACAAAGGAAAAATGTAAAGTACTTTATGCAAGCCATTGGAAGCTCTCTT	64280
QY	2336	CCCTCCATCTCTCATGTGGATGCTGAGGAATCTCAGATGGTGAACACTTTGATGCC	2395
DB	64281	CCCTCCATCTCTCATGTGAATGCTGCGGTATTAATCAGATTTTGAACACTTTGATGCC	64340
QY	2396	TAGATTTCTATTTCATCTCTCTCCCTACTCAGGACACTCGTGTGGATGGAATTTCTTG	2455
DB	64341	TAGATTTCTATTTCATCTCTCTCCCTACTCAGGACACTCGGTTGATTTGAATGGAATTTCTTG	64400

QY	2456	AGGAGATGCTTAACCTGGATTGAGCAGCTCACTCACTCAAGAGAGATCTACTATTATGAGGA	2515
DB	64401	AAGAGATGCTTAACCTGGATTGAGCAGCTCACTCACTCAAGAGAGATCTACTATTATGAGGA	64460
QY	2516	GCAAACTAAAGGAAGGTAAACCATGCTGATATTGGGGGCACTGCCCAACCTCATGTGTC	2575
DB	64461	GCAAACTAAAGGAAGGTAAACCATGCTGATATTGGGGGCACTGCCCAACCTCATGTGTC	64520
QY	2576	TTCACTCTTTATCGGAATGCTTACCTTTGGGAGAGAGCTAGTATTCAAAACAGGAGCATTTCC	2635
DB	64521	TTTATCTTTATTGGGAATGCTTACCTTTGGGAGAGAGCTAGTATTCAAAACGAGAGCATTTCC	64580
QY	2636	CAAACTCTTAGAACACATTTTCGATTTTATGAATTTGGATCAGCTAAGAGAGATCAGATTTGAGG	2695
DB	64581	CAAACTCTTAGAACACATTTTCGATTTTATCGAATTTGGATCAGCTAAGAGAGATGAGATTTGAGG	64640
QY	2696	ACGGCAGCTCACCCCTGTTTGGAAAAAGATAGAAATAGGCGAGTGCAGGTTGGAAATCTCGGGA	2755
DB	64641	ATGGCAGCTCACCCCTGTTTGGAAAAAGATAGAAATCTTCTGCTGCAGAGTTGGAAATCAGGGA	64700
QY	2756	TTTACTGGTATCATTTACCTTCCAAAGCTCAGGAGATTCGAATTAGATACGGAGATTAAG	2815
DB	64701	TTTATGGTATCATTTTCACTTCCAAAGCTCAGGAGATTTCACTTGAATCAAAAGTAAAG	64760
QY	2816	TGGCTGGGCTTGCTCAGCTCGAGGGAGAGTGAACGACACCCAAATCGCCCCGTGCTGC	2875
DB	64761	TGGCTAGGCTTGCTCAGCTGGAGGGAGAGTGAACACACCCAAATCGCCCCGTGCTGC	64820
QY	2876	TAATGTACAGTGACCGAAGGTATCAGCACTGGGGGGCTGAAGCCGAGAGATCTTCTATAG	2935
DB	64821	GAATGGACAGTGACCGAAGGTATCAGCACTGGGGGGCTGAAGCCGAGAGATCTTCTATAG	64880
QY	2936	AAGTGC AAAACAGCAGATCCTGTTCTCGATGCCGAAGGATCAGTCACTGTAGCAGTGGAAAG	2995
DB	64881	AAGTGC AAAACAGCAGATCCTGTTCTCGATGCCGAAGGATCAGTCACTGTAGCAGTGGAAAG	64940
QY	2996	CACCGGATCCCTTCCGAGCAGGAGGAGAGAGCTCCGAGTCCGAGGTGATCAGTTGA	3055
DB	64941	CACCGGATCCCTTCCGAGCAGGAGGAGAGAGCTCCGAGTCCGAGGTGATCAGTTGA	65000
QY	3056	CGACGAATGATAGCGAAG	3073
DB	65001	CGACGAACGATAGGTGATAG	65018

```

RESULT 8
US-10-437-963-37316
; Sequence 37316, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 37316
; LENGTH: 4596
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_41056C.1
US-10-437-963-37316
Query Match      82.8%; Score 2565.2; DB 7; Length 4596;

```

Best Local Similarity 98.3%; Pred. No. 0; Matches 2604; Conservative 0; Mismatches 43; Indels 3; Gaps 1;			
Qy	422	TTGACATGATTCCTATGAGAGACATTCGTAATCAGTCAGCTCGCAATGTCGATGAGG 481	
Db	29	TAGCAATAGATTCCTATGAGAGACATTCGCAATCAGTCAGCTCGCAATGTCGATGAGG 88	
Qy	482	CTGAGCTGTGTGGGTTTCTGATCTCAAGAAAGGCTCTTGAATGATCGATACCAATG 541	
Db	89	CTGAGCTGTGTGGGTTTCTGATCTCAAGAAAGGCTCTTGAATGATCGATACCAATG 148	
Qy	542	CTAATGATGTCGCGCAAGGTAATCTGTGTTGTTGGATGGGTGTTTAAAGCAAGACAG 601	
Db	149	CTAATGATGTCGCGCAAGGTAATCTGTGTTGTTGGATGGGTGTTTAAAGCAAGACAG 208	
Qy	602	CTCTTTGAGGAAGATCTTTGAAAGCAAGACATTTAGGAAGAACTTCCCTTGCATG 661	
Db	209	CTCTTTGAGGAAGATCTTTGAAAGCAAGACATTTAGGAAGAACTTCCCTTGCATG 268	
Qy	662	CTTGATTAAGTGCATCAATCAATTTCAAGGATGAGTACTTAAAGATATGATAGCC 721	
Db	269	CTTGATTAAGTGCATCAATCAATTTCAAGGATGAGTACTTAAAGATATGATAGCC 328	
Qy	722	AACCTTTGCCCCAGTTCTCTGGATCACTCTTGCAGAAATTCGAAGGAAGGTGGTG 781	
Db	329	AACCTTTGCCCCAGTTCTCTGGATCACTCTTGCAGAAATTCGAAGGAAGGTGGTG 388	
Qy	782	TGCAAGTACATCACTTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 841	
Db	389	TGCAAGTACATCACTTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 448	
Qy	842	TTGTTCTAGATGATCTATGATGATGATGATGATGATGATGATGATGATGATGATG 901	
Db	449	TTGTTCTAGATGATCTATGATGATGATGATGATGATGATGATGATGATGATGATG 508	
Qy	902	CTAAGAAATTAAGAGGAGTCTGATGATGATGATGATGATGATGATGATGATGATG 961	
Db	509	CTAAGAAATTAAGAGGAGTCTAATGATGATGATGATGATGATGATGATGATGATG 568	
Qy	962	AGAGTGTGCAAGCTCACTGTGTGATGATGATGATGATGATGATGATGATGATGAT 1021	
Db	569	AGAGTGTGCAAGCTCACTGTGTGATGATGATGATGATGATGATGATGATGATGAT 628	
Qy	1022	TAAATGCTGATGAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAA 1081	
Db	629	TAAATGCTGATGAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAA 688	
Qy	1082	TGCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1141	
Db	689	TGCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 748	
Qy	1142	CAATAGAGCTGTGCTGCAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 1201	
Db	749	CAATAGAGCTGTGCTGCAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 808	
Qy	1202	TTCCCTCAGAACTAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 1261	
Db	809	TTCCCTCAGAACTAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 868	
Qy	1262	GTTACAAACCACTCAATCCCAATTTGAAACCAATTTGATGATGATGATGATGATGAT 1321	
Db	869	GTTACAAACCACTCAATCCCAATTTGAAACCAATTTGATGATGATGATGATGATGAT 928	
Qy	1322	AGGATTTGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 1381	
Db	929	AGGATTTGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAG 988	
Qy	1382	GACCAAGGTTGGATGACGATTAAGGATGTCGAGAAAGTACTTAAATGAGCTAATCA 1441	
Db	989	GACCAAGGTTGGATGACGATTAAGGATGTCGAGAAAGTACTTAAATGAGCTAATCA 1048	
Qy	1442	ACCAAGTATGATTTCAAGATCAAGATGCGGATAGCAAGGAAATTAAGCTTGTGCA 1501	

Db	1049	ACCGAATGATGATTCACAGATCAAGAGTGGCATAGCAGGAAAAATTAAGACTTGTGCA 1108	
Qy	1502	TTCATGATATCATCGTGTATATCAAGTTTCAATCTCGAGACAGAAAAATTTTGTATAT 1561	
Db	1109	TTCATGATATCATCGTGTATATCAAGTTTCAATCTCGAGACAGAAAAATTTTGTATAT 1168	
Qy	1562	TACCAATGGAGATGCTCTGATTTAGTTTCAAGAAAAACATCGCCACATAGCAATCCATG 1621	
Db	1169	TACCAATGGAGATGCTCTGATTTAGTTTCAAGAAAAACATCGCCACATAGCAATCCATG 1228	
Qy	1622	GGAGTATGCTTGCAAAACTGATTTGAGTTGAGAGCATTTTTCGATCATTAAGCTATTTTG 1681	
Db	1229	GGAGTATGCTTGCAAAACTGATTTGAGTTGAGAGCATTTTTCGATCATTAAGCTATTTTG 1288	
Qy	1682	GTGACAGACCCAGAGTCTAGCAGATGAGTTTCTCGAGATCAATTCAGAGATGTTACGGG 1741	
Db	1289	GTGACAGACCCAGAGTCTAGCAGATGAGTTTCTCGAGATCAATTCAGAGATGTTACGGG 1348	
Qy	1742	TCTTGGATCTTGAAGATGTCATTTTAAATCACTCAAAAAGATTTTCGACCGTATTTGCAT 1801	
Db	1349	TCTTGGATCTTGAAGATGTCATTTTAAATCACTCAAAAAGATTTTCGACCATATTTGCAT 1408	
Qy	1802	TGTTGTGCACTTTGAAATCACTTGTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1861	
Db	1409	TGTTGTGCACTTTGAAATCACTTGTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1468	
Qy	1862	GATCCATTTGGTAAAATCAAGGCTTCAAAAATTTTGAACATGCGGAGCACATATTTGCAG 1921	
Db	1469	GATCCATTTGGTAAAATCAAGGCTTCAAAAATTTTGAACATGCGGAGCACATATTTGCAG 1528	
Qy	1922	CAGTCAAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1981	
Db	1529	CAGTCAAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1588	
Qy	1982	TTCAATTTACCAACTTTTGTCTGATGATGATGATGATGATGATGATGATGATGATG 2041	
Db	1589	TTCAATTTACCAACTTTTGTCTGATGATGATGATGATGATGATGATGATGATGATG 1648	
Qy	2042	TGCTTAAAGTATTCACACTTTTGTAGTGTGATGATGATGATGATGATGATGATGATG 2101	
Db	1649	TGCTTAAAGTATTCACACTTTTGTAGTGTGATGATGATGATGATGATGATGATGATG 1708	
Qy	2102	TGCACATGCGCAACCAAGTTTGTCTGATGATGATGATGATGATGATGATGATGATG 2161	
Db	1709	TGCACATGCGCAACCAAGTTTGTCTGATGATGATGATGATGATGATGATGATGATG 1768	
Qy	2162	TAGGTAAGTTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2221	
Db	1769	TAGGTAAGTTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1828	
Qy	2222	GAGCAATCAAGAGCTGGGCGAGTTTAAAGCAAGCTGAGGAAATTTAGGTTGTCACAAACG 2281	
Db	1829	GAGCAATCAAGAGCTGGGCGAGTTTAAAGCAAGCTGAGGAAATTTAGGTTGTCACAAACG 1888	
Qy	2282	GGTTCGCAAGGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2341	
Db	1889	GGTTCGCAAGGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1948	
Qy	2342	AATCTCTCAATGTCGAGATGTCGAGAAATCTCAG--ATGTTGGAACACTTGTGTCCTAG 2398	
Db	1949	AATCTCTCAATGTCGAGATGTCGAGAAATCTCAG--ATGTTGGAACACTTGTGTCCTAG 2008	
Qy	2399	ATTCTATTTTCACTCTCTCCCTTAAAGCACTGAGGAAATTTGATGATGATGATGATG 2458	
Db	2009	ATTCTATTTTCACTCTCTCCCTTAAAGCACTGAGGAAATTTGATGATGATGATGATG 2068	
Qy	2459	AGATGCTTAACTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2518	
Db	2069	AGATGCTTAACTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2128	
Qy	2519	AACCTAAAGGAAAGTAAACCACTGTCATGATGATGATGATGATGATGATGATGATG 2578	
Db	2129	AACCTAAAGGAAAGTAAACCACTGTCATGATGATGATGATGATGATGATGATGATG 2188	

QY 2579 ATCTTTATCGAATGCTTACCTTGGGAGAACTAGTATTCAAACAGGAGCATTCCTCAA 2638  
DB 2189 ATCTTTATCGAATGCTTACCTTGGGAGAACTAGTATTCAAACAGGAGCATTCCTCAA 2248  
QY 2639 ATCTTAGAACACCTTTGGATTATGAAATTCGATCACTAAGAGAGATCAGATTTGAGGAGC 2698  
DB 2249 ATCTTAGAACACCTTTGGATTATGAAATTCGATCACTAAGAGAGATCAGATTTGAGGAGC 2308  
QY 2699 GCAGCTCACCCCTGTTGGAAAAGATAGAAATAGGCGAGTGCAGGTTGGATCTGGGATTA 2758  
DB 2309 GCAGCTCACCCCTGTTGGAAAAGATAGAAATAGGCGAGTGCAGGTTGGATCTGGGATTA 2368  
QY 2759 CTGGTATCAATTCACCTTCCAAAGCTCAAGGAGATTCCTCAATTAGATACGGAAGTAAAGTGG 2818  
DB 2369 TTGGTATCAATTCACCTTCCAAAGCTCAAGGAGATTCCTCAATTAGATACGGAAGTAAAGTGG 2428  
QY 2819 CTGGGCTTGTGAGCTGGAGGAGAGTGAACGACACCCAAATCGCCCGTGTGCTAA 2878  
DB 2429 CTGGGCTTGTGAGCTGGAGGAGAGTGAACGACACCCAAATCGCCCGTGTGCTAA 2488  
QY 2879 TGTAAGTGAACCAAGGTATACGACCTGGGGGCTGAAGCCGAAAGGATCTTCTATAGAAG 2938  
DB 2489 TGTAAGTGAACCAAGGTATACGACCTGGGGGCTGAAGCCGAAAGGATCTTCTATAGAAG 2548  
QY 2939 TGCAACAGCAGATTCCTGTTCTGTATGCCGAAGGATCAGTCACTGTAGCAGTGGAGCAA 2998  
DB 2549 TGCAACAGCAGATTCCTGTTCTGTATGCCGAAGGATCAGTCACTGTAGCAGTGGAGCAA 2608  
QY 2999 CGGATCCCTTCCGAGCAGGAGGAGAGAGCTCGCAGTCCGAGTGTATCACTGTAGCAGT 3058  
DB 2609 CGGATCCCTTCCGAGCAGGAGGAGAGAGCTCGCAGTCCGAGTGTATCACTGTAGCAGT 2668  
QY 3059 CGAATGATAG 3068  
DB 2669 CGAATGATAG 2678

## RESULT 9

US-10-656-394A-11

; Sequence 11, Application US/10656394A

; Publication No. US20040210957A1

; GENERAL INFORMATION:

; APPLICANT: Wang et al.

; TITLE OF INVENTION: Cloning and Characterization of the

; FILE REFERENCE: broad-spectrum resistance gene Pi2

; CURRENT FILING DATE: 2003-09-05

; SOFTWARE: FastSeq for Windows Version 4.0

; NUMBER OF SEQ ID NOS: 16

; SEQ ID NO 11

; LENGTH: 2997

; TYPE: DNA

; ORGANISM: Oryza minuta

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2997)

US-10-656-394A-11

Query Match

Best Local Similarity 77.2%; Score 2393.6; DB 8; Length 2997;

Matches 2453; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 422 TTGACATGGAATTCCTATGCGAAGACATTCGTAATCAGTCCGATCGCAATGTGGATGAGG 481

DB 197 TAGCAATAGATTCCTATGCGAAGACATTCGCAATCAATCAGTCCGAATGTGGATGAGG 256

QY 482 CTGAGCTTGTGGGTTTCTGACTCCAGAAAGGCTGCTTGAATATGATCGATACCAATG 541

DB 257 CTGAGCTTGTGGGTTTCTGACTCCAGAAAGGCTGCTTGAATATGATCGATACCAATG 316

QY 542 CTAATGATGTCGGCCCAAGGTAAATCTGTGTTGGGATGGGTGTTAGGCGAAGACAG 601

DB 317 CTANTGATGCTCGGCGAAGGTAACTGTGTGTTGGATGGGTGTTTAGGCAAGACAG 376  
QY 602 CTCTTTGAGGAGATCTTTGAAAGCGAAGACATTTAGGAACATCTCCCTTGCATG 661  
DB 377 CTCTTTGAGGAGATCTTTGAAAGCGAAGACATTTAGGAACATCTCCCTTGCATG 436  
QY 662 CTGGAATACAGTGCACATCACTTTACAGGATTCAGCTACTTAAAGATATGATACGCC 721  
DB 437 CTGGAATACAGTGCACATCACTTTACAGGATTCAGCTACTTAAAGATATGATACGCC 496  
QY 722 AACTTTGGCCCCAGTTCTCTGGAATCAACTCTTGCAGAAATTCGAAGGAGGAGTGGTGG 781  
DB 497 AACTTTGGCCCCAGTTCTCTGGAATCAACTCTTGCAGAAATTCGAAGGAGGAGTGGTGG 556  
QY 782 TGCAGATCATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGGAGGAGTACTTTG 841  
DB 557 TGCAGATCATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGGAGGAGTACTTTG 616  
QY 842 TTGTTCTAGATCATCTATGGAATTTTCAATGATTCGAATTCGATTAATGAAATTCGATTTTC 901  
DB 617 TTGTTCTAGATCATCTATGGAATTTTCAATGATTCGAATTCGATTAATGAAATTCGATTTTC 676  
QY 902 CTAAGAAACAATAAGAGGCGCAGTCGAATAGTAAATAACACTCGGAATGTGTGATCTTGGCG 961  
DB 677 CTAAGAAACAATAAGAGGCGCAGTCGAATAGTAAATAACACTCGGAATGTGTGATCTTGGCG 736  
QY 962 AGAAGTGTGCCACAGCTCACTGAGTGTACCACTTGTGATTTCTTGCAGATGAACGATGCCA 1021  
DB 737 AGAAGTGTGCCACAGCTCACTGAGTGTACCACTTGTGATTTCTTGCAGATGAACGATGCCA 796  
QY 1022 TAACATTTGCTACTGAGAAAACAATAAATCATGAGACATGGAATCAATAAATAAATA 1081  
DB 797 TAACATTTGCTACTGAGAAAACAATAAATCATGAGACATGGAATCAATAAATAAATA 856  
QY 1082 TGCAAAAGATGTTGAACGAAATTTGTAATAAATGTTGTCGCTCTACCAATAGCAATCTTA 1141  
DB 857 TGCAAAAGATGTTGAACGAAATTTGTAATAAATGTTGTCGCTCTACCAATAGCAATCTTA 916  
QY 1142 CAATAGGAGCTGTCTGCACTAAACAGGTGTGAGAAATGGGAGAAATTCATGAACACC 1201  
DB 917 CAATAGGAGCTGTCTGCACTAAACAGGTGTGAGAAATGGGAGAAATTCATGAACACC 976  
QY 1202 TTCCTTTAGAACTAGAAATAAACCAGCTTGAAGCTTTGAGGAGAAATGGTCACTAG 1261  
DB 977 TTCCTTTAGAACTAGAAATAAACCAGCTTGAAGCTTTGAGGAGAAATGGTCACTAG 1036  
QY 1262 GTTACCAACCACTACCTCCCATTTGAAACCACTCTTTGATCTAAGTATCTTCTCCTG 1321  
DB 1037 GTTACCAACCACTACCTCCCATTTGAAACCACTCTTTGATCTAAGTATCTTCTCCTG 1096  
QY 1322 AGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGATCGATAGCAAGAGGTTTGTTA 1381  
DB 1097 AGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGATCGATAGCAAGAGGTTTGTTA 1156  
QY 1382 GACCAAGGTTGGGATGAGCTAAGGATTCGAGAGAAATGTTAATGAGCTAATCA 1441  
DB 1157 GACCAAGGTTGGGATGAGCTAAGGATTCGAGAGAAATGTTAATGAGCTAATCA 1216  
QY 1442 ACCGAAGTATGATTAACAGATCAAGAGTGGCATAGCAGGAAAAATTAAGACTTGTGCA 1501  
DB 1217 ACCGAAGTATGATTAACAGATCAAGAGTGGCATAGCAGGAAAAATTAAGACTTGTGCA 1276  
QY 1502 TTCAATGATCATCGTGTATCATCACTTCAATCTCGAGACAGGAAAAATTTGTATTAT 1561  
DB 1277 TTCAATGATCATCGTGTATCATCACTTCAATCTCGAGACAGGAAAAATTTGTATTAT 1336  
QY 1562 TACCAATGGGAGATGGCTCTGATTTAGTTTCAAGAAAAACACTCGCCACATAGCAATCCATG 1621  
DB 1337 TACCAATGGGAGATGGCTCTGATTTAGTTTCAAGAAAAACACTCGCCACATAGCAATCCATG 1396  
QY 1622 GGAGTATGCTTCGCAAACTGGAATTCGAGCAATTTTCCGATCATAGCTATTATTG 1681





361 QY GAAGTGTAGCAGGACACACGCTTGTAGTCAAGCTATTCTCTGGCACAGAG 420  
538 Db GAAGTGTAGCAGGAACTCAGCTACATTTAGTCAAACCTATTTCATCCAGCAATGAG 597  
421 QY ATTGACATGGAATCCTATGACAGAGACATTCGTAATCAGTCACTCGCAATGTGGATGAG 480  
598 Db GATGACATGGAATGTTACGACAGAGACATTCGTAATCAGTCACTAGCAATGTAGATGAA 657  
481 QY GCTGAGCTTGTGGGTTTCTGACTCCAGAGAAAGGCTGCTGGAATGATCGATACCAAT 540  
658 Db ACTGAGCTTGTGGGTTTCTGACTCTAAGTA----- 690  
541 QY GCTAATGATGTCGCGCCAAAGGTAATCTGTGTTGTTGGGATGGTGGTTTAGGCAAGACA 600  
691 Db ----- 690  
601 QY GCTCTTTCGAGGAGATCTTTGAAAGCGAGAGACATTTAGGAAGAACTTCCCTTGGCAAT 660  
691 Db ----- 690  
661 QY GOTTGGATTACAGTGTCAATCATTTACAGGATTGAGCTACTTAAAGATATGATAGCG 720  
691 Db -----AGGATTGAGCTACTCAAAGATATGATAGCG 720  
721 QY CAACTTCTTGGCCCCAGTCTCTGGATCAACTCTCGAAGAACTTCGAAGAACTCAAGGAGAGTGGTG 780  
721 Db CAAATTCCTAGGTTCCAAATCACTGGATCAAGTCTTCGAAGAACTTCGAAGAACTCAAGGAGAAATGGTG 780  
781 QY GTGCAAGTACATCATCTTTCTGAGTACTCTGATAGAGAGCTCAAGGAGAGAGGTACTTTT 840  
781 Db GTGCAAAATACCTCATCTTTCTGACTACTTGAGAGAAAAGCTCAAGGAGAAAGAGGTATTTT 840  
841 QY GTTGTCTAGATGATCTATGGAATTTACATGATGGAATGGAATGGAATGGAATGGAATGGAATTT 900  
841 Db GTTGTCTAGATGATCTATGCTTTTGTAGATGCAATGGAATGGAATGGAATGGAATGGAATTT 900  
901 QY CCTAAGAACAAATAGAGAGGCGAGTGAATAGTAATTAACCACTCGGAATGTTGATCTTGGC 960  
901 Db CCTAAGATATACAAATAGGCGAGTCGGATGTTAGTAACCAACAGAGATGTTGGTCTAGCC 960  
961 QY GAGAGTGTGCGACAGCTCTAGTGTACCACTTGTATTTCTTCAGATGAACGATGCC 1020  
961 Db GAGAGTGTACCAACACTTCCCTAGTCTACCATCTTTGAAACATCTTCAGATGAATGATGCC 1020  
1021 QY ATAACTTTGCTACTGAGAGAAAACAAATATAAAATCATGAAGACATGGAATCAAAATAAAAT 1080  
1021 Db ATAACTTTGCTACTGAGAGAAAACAAATAGAACATGAGACATGGAAGACAAACAAAT 1080  
1081 QY ATGCAAAAGATGTTGAACGAAATGTAATAATGTTGGTCTACCAATTTAGCAATACTT 1140  
1081 Db ATGCAAAAAATAGTTGAACAAATTTGTAATAATGTTGGTCTACCAATTTAGCAATACTT 1140  
1141 QY ACAATAGAGCTGTGCTTGCATTAACAGGCTGCAAGATGGGAGAAATTTCTATGAACAC 1200  
1141 Db ACAATAGAGCTGTGTTGGCACTTAACAGATTTTAGAATGGGAGAAATTTTATAAACAG 1200  
1201 QY CTTCTTCAGAACTAGAAAATAAACCAAGCTCGAAGCTTTGAGAGAAATGGTGACCTTA 1260  
1201 Db CTTCTTCAGAACTTGAAGCAACCAAGCTTTCAAGCTTTGAGAGAAATGGTGACCTTT 1260  
1261 QY GTTTACAAACCACTTACCATCCATTTGAAACCACTGCTTTTGTATCTAAGTATCTTTCT 1320  
1261 Db GCTTACAAACCACTTACCATCTCATCTGAATCATGCTTTTGTACCTAAGTATCTTTCT 1320  
1321 QY GAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGATGATGAGAGAGGTTGTT 1380  
1321 Db GAGGATTTTGAATCAAAAGGAGTCTGCTTGTAGACAGATGATGATGAGAGGTTGTT 1380  
1381 QY AGACCAAAAGGTTGGATGACGACTAAGGATGTCGAGAGAAAGTTACTTTTAATGAGCTAATC 1440  
1381 Db AGACCAAAAGGTTGGATGACGACCAAGATGTTGGGACAGTTACTTTTAATGAGCTAATC 1440  
1441 QY AACCGAAGTATGATTTCAACGATCAAGAGTGGGCAATAGCGGAAATTAAGACTTGTGCA 1500

1441 Db AACCGAAGTATGATTTCAAAGATCAAGAGTGGGCATAGAAAGGAAATTTAAGAGTTGCCGA 1500  
1501 QY ATTCAATGATATCATCGTGATATCATAGTTTCAATCTCGAGACAGGAAATTTTGTATTA 1560  
1501 Db GTCCATGATATCATCGTGATATCATAGTTTCAATCTCTAGAGAGGAGAACTTTGTATTC 1560  
1561 QY TTACCAATGGAGATGGCTCTGATTTAGTTTCAAGGAAAAACCTCGCCACATAGCAATTCAT 1620  
1561 Db TTACCAATGGAGATGGCTCTGATTTCAATCTAGCACAGGAAAAACCTCGCCACATAGCAATTCAT 1620  
1621 QY GGGAGTATGCTTCCGAAAACTGGATTTGGAGCATTTTCGATCAATAGCTATTTT 1680  
1621 Db GGGAGCATGTCCTTCCGAAAAACAGGATTTGGAGCATTTTCGATCAATAGCTATTTT 1680  
1681 QY GGTGACAGACCCCAAGAGTCTAGCACATGCAATGTTTCTCCAGATCAATTTGAGGATGTTACGG 1740  
1681 Db GGTGACAGACCCCAATTAATCTAGCACACACTATTTCTCAATTAATTTCAAGATGTTACGG 1740  
1741 QY GTCTTGGATCTGGAAGATGTGACATTTCTTAATCACTCAAAAAGATTTTCGACGTTATGCA 1800  
1741 Db GTCTTGGATCTGGAAGATGTGAAATTTTAATCAACAAAAAGATTTTCAACAAATATAGCA 1800  
1801 QY TTGTTGTGCCACTTTGAAATACTTTGAGTATTGG-----ATATTCTCATTCATATTTCA 1854  
1801 Db TTGTTGTGCTCACTTTGAAATACTTTGAGTATTGGAGAAATTTCTCATCATGATATATACT 1860  
1855 QY CTTCCAGATCCATTTGGTAAACTTAAGGCTTACAACTTTTGAACATCCGAGGACATATAC 1914  
1855 Db CTTCCAGATCTATTTGGTAAATTTACATGCTTTACAGACCTTTGAATATGTCAAGTACATAC 1920  
1915 QY ATTGACGACCTACCAAGTGTGAGTCAAGTAACTTCCAAATCTCTGCACTCTCTCTGTTGATA 1974  
1921 Db ATTGACACACTACCAAGTGTGAGTCAAGTAACTTCCAAATCTCTGCGCACTCTCTCTGTTGATA 1980  
1975 QY GGACAGTTTCAATTTATGACAACTTTTGTCTAAACCAACCAATGGAAGTGAATTAACACACA 2034  
1981 Db AGGATATCTAATAATAACAAATTTTAGTATAAATATCAACCGGTGAAGTGTAACTAAACACA 2040  
2035 QY ATATGCTGCTTAAAGTATTTCACCTTTTGTAGTTAGTTCGCGATGATGCGTGAACAAAT 2094  
2041 Db ATGTTCTGCTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2100  
2095 QY GCTGAATTTGACATGCGCCACCAAAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2154  
2101 Db GCTGAATTTGACATGCGCCACCAAAAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
2155 QY AAAGCAATAGTAAAGTGTGCGAGACTTTGCAAGTGTCTAGAGTATGTAGATATCAGCGGAC 2214  
2161 Db AAAGTATAGGCAAGTGTGCGAGACTTTGCAAGTGTCTAGAGTATGTAGATATCAGCGGAC 2220  
2215 QY AGTAGTAGCAATCAAAAGAGCTGGGGCAGTTTAAAGCAAGCTGAGGAAATTTAGGTGTGACA 2274  
2221 Db AGTAGTAGCAATCAAAAGAGTGGGGCAGTTTAAAGCAAGCTGAGCTAAATTTAGGTGTGACA 2280  
2275 QY ACAAAGGCTGCAAAAGGAAAAATGTAAGTACTTTTATGAGCACTTTTATGAGCAAGCTCTCT 2334  
2281 Db ACAAAGGCTGCAAAAGGAAAAATGTAAGTACTTTTATGAGCACTTTTATGAGCAAGCTCTCT 2340  
2335 QY TCCCTCCAAATCTCTCCATGTGAGATGCTGCAAGAAATCTCAGATGTTGGGAACTCTTGAAGTGC 2394  
2341 Db TCCCTCCAAATCTCTCCATGTGAGATGCTGCAAGAAATCTCAGATGTTGGGAACTCTTGAAGTGC 2400  
2395 QY CTAGATTTCTATTTCT 2454  
2401 Db CTAGATTTCTATTTCT 2460  
2455 QY GAGGAGATGCTTAACCTGAGTGTGAGCAGCTCACTCACTGAGGAAAGATCTACTTTATGAGG 2514  
2461 Db GAGGAGATGCTTAACCTGAGTGTGAGCAGCTCTCGCACCTCACTGAGGATTTCTACTTTATGAGG 2520  
2515 QY AGCAAACTAAAGGAGGTAAGAAACCAATGCTGATGATTTGGGGCACTGCGCACTCATGTC 2574

Db 2521 AGTAACTAAAGAGGAAACCAATGCTGATCTTGGGCAATGGCCACCTCATGCTG 2580  
 Qy 2575 CTTTCATCTTTATCGGAATGCTTACCTTGGGAGAGCTAGTATTTCAAAACAGAGCAATTC 2634  
 Db 2581 CTTTGTCTTTCACTTGATGCTTACCTCGGGGAGAACTAGTATTTCAGAAACAGAGCAATTC 2640  
 Qy 2635 CCAATCTTTAGAACACTTTGGATTTATGAATGGATGATGCTTGAAGAGATCAGATTTGAG 2694  
 Db 2641 CAAAAGCTCAGGACACTTTGGTTTGAACAAGTGGATGCTTGAAGAGATGAGTTGAG 2700  
 Qy 2695 GACGCGAGCTCACCTCTGTTGAAAAGATAGAAATGAGCGAGTGCAGGTTGGAATCTGG 2754  
 Db 2701 AACGACAGCTCGCCCTATTGGAAGAAGATAGAAATGAGCGAGTGCAGGTTGGAATCTGG 2760  
 Qy 2755 ATTACTGGTATCAATTCACCTTCAAGCTCAAGGATTCGAATAGATAGCAAGTAA 2814  
 Db 2761 ATTATTGGTATCTTAACCTTATGAGGCTAAAGGAATTAACATTTGATACAGAGTTAA 2820  
 Qy 2815 GTGGCTGGGCTTGGTCAAGCTGAGGAGAGAGTGAACGACACACCCAAATCGCCCGTGTG 2874  
 Db 2821 GTTGGTTATCTTGGTCAAGTGGAAAGAGAGTGGGACACACCCAAATCGCCCGTGTG 2880  
 Qy 2875 CTAATGTAAGTACGCAAGAGTATCAGACCTGGGGGCTGAAGCGAGGATCTTCTATA 2934  
 Db 2881 CGTATGAGGAGGACGCAAGCTGTCAAGCTTGAAGGAGGATGCAAGAGGATCAGCTGTA 2940  
 Qy 2935 GAAGTGCAACACAGACATCTGTCTGATGCCGAAGAT 2974  
 Db 2941 GAATGGAGCAACGAGGCCCTCCTGAGCCGAGAGCT 2980

RESULT 11

US-10-656-394A-15  
 ; Sequence 15, Application US/10656394A  
 ; Publication No. US20040210957A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang et al.  
 ; TITLE OF INVENTION: Cloning and Characterization of the  
 ; TITLE OF INVENTION: broad-spectrum resistance gene P12  
 ; FILE REFERENCE: 035718/252062  
 ; CURRENT APPLICATION NUMBER: US/10/656,394A  
 ; CURRENT FILING DATE: 2003-09-05  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 15  
 ; LENGTH: 2422  
 ; TYPE: DNA  
 ; ORGANISM: Oryza minuta  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: 2014, 2043, 2099, 2114, 2154, 2172, 2178, 2199, 2205, 2226,  
 ; LOCATION: 2268, 2299, 2333, 2337, 2359, 2356  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-10-656-394A-15

Query Match 52.3%; Score 1621; DB 8; Length 2422;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1479 AGGAAAAATTAAAGACTTGTGCAATTCATGATATCATCGGTGATATCAAGTTCAATCTC 1538  
 Db 1 AGGAAAAATTAAAGACTTGTGCAATTCATGATATCATCGGTGATATCAAGTTCAATCTC 60  
 Qy 1539 GAGACAGGAAAAATTTGTATTATTACCAATGGAGATGGCTCTGATTTAGTTTCAAGAAAA 1598  
 Db 61 GAGACAGGAAAAATTTGTATTATTACCAATGGAGATGGCTCTGATTTAGTTTCAAGAAAA 120  
 Qy 1599 CACTCGCCACATAGCAATTCACCGAGATGTCCTGCAAACTGATTTGATTTGAGATTCAGCAT 1658  
 Db 121 CACTCGCCACATAGCAATTCACCGAGATGTCCTGCAAACTGATTTGATTTGAGATTCAGCAT 180  
 Qy 1659 TATTGATCATTAGCTATTGTTGTCAGACAGCCAGAGCTTAGCACATGAGTTTGTCC 1718

Db 181 TATTCGATCATTTAGCTATTTTGGTGACAGACCCAGAGCTTAGCACATGCACTTGTGTC 240  
 Qy 1719 AGATCAATTCAGGATGTTACGGGTCTTGGATCTTGAAGATGTGACATCTTCTTAATCACTCA 1778  
 Db 241 AGATCAATTCAGGATGTTACGGGTCTTGGATCTTGAAGATGTGACATCTTCTTAATCACTCA 300  
 Qy 1779 AAAAGATTTCCGACCCCTATTGCAATTTGTTGTGCACTTGAATACCTTGAATATCTGATATTC 1838  
 Db 301 AAAAGATTTCCGACCCCTATTGCAATTTGTTGTGCACTTGAATATCTGATATTC 360  
 Qy 1839 GTCAATCCATPATTTCACTTCCAGATCCATTTGTTGAATACCTTGAATATCTGATATTC 1898  
 Db 361 GTCAATCCATPATTTCACTTCCAGATCCATTTGTTGAATACCTTGAATATCTGATATTC 420  
 Qy 1899 CATGCCGAGCACAATACATTTGAGCAGCTTACCAAGTGAGATCAGTAAATCTCCTGCTGCA 1958  
 Db 421 CATGCCGAGCACAATACATTTGAGCAGCTTACCAAGTGAGATCAGTAAATCTCCTGCTGCA 480  
 Qy 1959 TACTTCTCTTGTATGAGCAGCTTTCATATGACAACTTTAGTCTAAACCCCAATGAA 2018  
 Db 481 TACTTCTCTTGTATGAGCAGCTTTCATATGACAACTTTAGTCTAAACCCCAATGAA 540  
 Qy 2019 GTGCATAAATAACACATATGCTGCTTAAAGTATTCACACCTTTAGTCTGCGATGA 2078  
 Db 541 GTGCATAAATAACACATATGCTGCTTAAAGTATTCACACCTTTAGTCTGCGATGA 600  
 Qy 2079 TCGTGCAAAAACAAATTTGCTGAATTTGACATGGCCACCAAAAGTTGCTGCTGATCAAT 2138  
 Db 601 TCGTGCAAAAACAAATTTGCTGAATTTGACATGGCCACCAAAAGTTGCTGCTGATCAAT 660  
 Qy 2139 CGGTGTGAAGGTACCCCAAGGAATAGTGTGCGAGACTTGCAGAGCTTCTAGAGTATGT 2198  
 Db 661 CGGTGTGAAGGTACCCCAAGGAATAGTGTGCGAGACTTGCAGAGCTTCTAGAGTATGT 720  
 Qy 2199 AGATATCAGCGGACGAGCTAGTAGAGCAATCAAGAGCTGGGCGAGTTAAGCAAGCTGAG 2258  
 Db 721 AGATATCAGCGGACGAGCTAGTAGAGCAATCAAGAGCTGGGCGAGTTAAGCAAGCTGAG 780  
 Qy 2259 GAAATTTAGGTGTGACAAACAGGGTCCACAAAGGAAATGTAAGATCTTTTATGCGC 2318  
 Db 781 GAAATTTAGGTGTGACAAACAGGGTCCACAAAGGAAATGTAAGATCTTTTATGCGC 840  
 Qy 2319 CATTGAGAAAGCTCTCTTCTCCCAATCTCTCCATGTGATGCTGCAGGAATCTCAGATGG 2378  
 Db 841 CATTGAGAAAGCTCTCTTCTCCCAATCTCTCCATGTGATGCTGCAGGAATCTCAGATGG 900  
 Qy 2379 TGGAACTAGTGTGCTAGTATCTTATTTCTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCT 2438  
 Db 901 TGGAACTAGTGTGCTAGTATCTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960  
 Qy 2439 GTTGGATGGAATTTCTTGGAGAGATGCTTAACTGGATTTGAGCAGCTCTCACTCACTGAA 2498  
 Db 961 GTTGGATGGAATTTCTTGGAGAGATGCTTAACTGGATTTGAGCAGCTCTCACTCACTGAA 1020  
 Qy 2499 GATCTACTTATTTGAGGAGCAAACTAAAGAGATGCTTAACTGGATTTGAGCAGCTCTCT 2558  
 Db 1021 GATCTACTTATTTGAGGAGCAAACTAAAGAGATGCTTAACTGGATTTGAGCAGCTCTCT 1080  
 Qy 2559 GCCCAACCTCATGCTCTTCTCTTATCGGAATGCTTACCTTGGGAGAGCTAGTATTT 2618  
 Db 1081 GCCCAACCTCATGCTCTTCTCTTATCGGAATGCTTACCTTGGGAGAGCTAGTATTT 1140  
 Qy 2619 CAAAAAGAGGAGCAATTTCCCAATCTTATAGAACACTTTGGATTTATGAATTTGATCAGCT 2678  
 Db 1141 CAAAAAGAGGAGCAATTTCCCAATCTTATAGAACACTTTGGATTTATGAATTTGATCAGCT 1200  
 Qy 2679 AGAGATCAGATTTGAGGAGCGAGCTCACCCCTGTTGGAAGATAGAAATAGCGGAGTG 2738  
 Db 1201 AGAGATCAGATTTGAGGAGCGAGCTCACCCCTGTTGGAAGATAGAAATAGCGGAGTG 1260  
 Qy 2739 CAGTTGGAAATCTGGATTTACTGGTATCATTTCCCTTCAAGCTCAAGGAGATTTCAAT 2798  
 Db 1261 CAGTTGGAAATCTGGATTTACTGGTATCATTTCCCTTCAAGCTCAAGGAGATTTCAAT 1320

298 AAGCTAAAGGATCGCCATCGGATTCGCAATCCAGATCCGCAATCTCAGGACAAGAAATTGAA 357  
 361 GAAGTCAGTAGCAGAGAACACACGCTTACAGTTTGTAGTCAAGCT---ATTCTCTGGCACA 417  
 358 GAAGTAGCAGTAGGAACTAGCTTACACTTAATAGAGATGACCTCAGCTGCACCACT 417  
 418 GAGATTGACATGGATTCCTATCGAGAAGACATTCGTATATCAGTCAGCTCGAATGTGGAT 477  
 418 ACTGATGAGAGAAATTTATTTATGGAAGACATTCGCAACCAATAAGCTAAACAACATTGAG 477  
 478 GAGGCTGAGCTTGTGGGTTTCTGACCTCCAAAGAAAGGCTGCTTGAATAATGATCGATACC 537  
 478 GAAGCTGATCTTGTGGGTTTCTGACCCCAAAAGAGAGTTGCTTGTATCTTATAGATGTC 537  
 538 AATGCTTAATGATGGTCCGCGCAAGGTAATCTGTGTGTGGATGGGTGTTTGGGATG 597  
 538 CATGCCAATGACGGACCTACAAAGTTGTATGTGTGTGGTATGGGTGTTTGGGTAAG 597  
 598 ACAGCTCTTTCGAGGAGATCTTTGAAAGCCAAAGACATCTAGGAGAACTTCCCTTGC 657  
 598 ACTACTATTTGCAAGGAAATTTATGAAAGCAAGAGGACATTCGAAAGAAATTTTCTTGC 657  
 658 AATGCTTGGATTACAGTGTCAATCATTTTCAAGGATTTGAGCTATCTTAAGATATGATA 717  
 658 TGTGCTTGGATTACTTGTTCACAGTCTTGTAGGTTGGAATCTACTCAAGGATTTGATG 717  
 718 CGCCAACTTCTTGGCCCGGCTTCTGATCACTCTTGAAGAAATTTGCAAGGAGGAGTG 777  
 718 GTGAAATCTTTTGGAGAGAGAGTACTGAAAGAGCGGCTGAGAGAGAA---G 774  
 778 GTGGTCAAGTACATCATCTTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGAGTAC 837  
 775 GTTCCACAGTAGACGACCTCGCAGTACCTCAGGACAGAGTTAAATGAAGAGAGTAC 834  
 838 TTTGTTGTTCTAGATGATCTATGATTTTACATGATTTGGAATTTGGAATTAATGAATGCA 897  
 835 TTTGTTGTTCTGATTAACGTTGAGGAGTACAGATTCATGGAATTTGGAATTAATGATGTC 894  
 898 TTTCTTAAGAACAAATAAGAGGAGGAGTCAAGATAGTAATTAACCACTCGGAATTTGATCTT 957  
 895 TTCCCTAGAAATAACAAATAAGAGGAGCGGCTGATAGTAACCAAGAGAGATTTGGCTTA 954  
 958 GCGGAGAGTGTGCGCACAGCTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1017  
 955 ACTAAGGAGTGTACTTCTGAAATGCTTATCTACAGCTTAAACCCCTAGAAATAAACAT 1014  
 1018 GCATTAACATTTGCTACTGAGAAAAACAAATAAAATCATGAAGACATGGAATCAAAATAAA 1077  
 1015 GCAAGAGATTTGCTTCTACGGAAGCAATTAAGCAATAGGAGATATGGAAGATGATAAA 1074  
 1078 AATATGCAAAAGATTTGAGCAAGATTTGTAATTAATTAATTAATTAATTAATTAATTAAT 1137  
 1075 AAGATGAGTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1134  
 1138 CTTACAAATAGGAGTGTGCTTCAACTAAACAGGTGTCAGAAATGGAAGAAATTTCTATGAA 1197  
 1135 CTCAATATAGGAGGCTGCTTCAACCAAGAGATAGAGAGTGGGAACTTTTATAGT 1194  
 1198 CACTTCTTCTAGAACTAGAAATAAACCAAGCTTGGAGCTTTGAGAGAGATGAGTGAAC 1257  
 1195 CAGATACCTTCAAGGCTGAGAGCAACCAACCTTGAAGCAATGGAAGAGATGAGTGAAC 1254  
 1258 CTAGGTTTCAACCACTTACCTCCATTTGAAACCAATGCTTTTGTATCTAAGTATCTTT 1317  
 1255 CTAAATTAACATCTTACCTGCTCATCTTAAGCAATGCTTTTGTATCTAAGCATATTT 1314  
 1318 CTTGAGATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1377  
 1315 CTTGAGATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1374  
 1378 GTTAGACCAAGGTTGGGATGACGACTAAGGATGTGGAGAAAGTACTTTAATGAGCTA 1437  
 1375 ATTAAAGCTAGGACTAATATGACTATTGAGATGTTGGGAAAGATTTACTTTAAGACATT 1434

2799 TAGTACGGAAGTAAGTGGCTGGCTGGTTCAGCTGAGGAGGAGTGAACGACACCC 2858  
 1321 TAGATACGGAAGTAAGTGGCTGGCTGGTTCAGCTGAGGAGGAGTGAACGACACCC 1380  
 2859 AAATCGCCCGCTGCTCTAATGTACAGTGAACGGAAGTATCACCACTGGGGCTGAAGC 2918  
 1381 AAATCGCCCGCTGCTCTAATGTACAGTGAACGGAAGTATCACCACTGGGGCTGAAGC 1440  
 2919 CGAAGGATCTTATAGAGTGAACGAGATCTGCTGATGATGATGATGATGATGATGATGAT 2978  
 1441 CGAAGGATCTTATAGAGTGAACGAGATCTGCTGATGATGATGATGATGATGATGATGAT 1500  
 2979 CACTGTAGCAGTGAAGCAACGATCCCTTCCGAGCAGGAGGAGGAGCTCGCAGTC 3038  
 1501 CACTGTAGCAGTGAAGCAACGATCCCTTCCGAGCAGGAGGAGGAGCTCGCAGTC 1560  
 3039 GCAGGTGATCAGCTTGAAGCAACGATGATGATGATGATGATGATGATGATGATGATGAT 3098  
 1561 GCAGGTGATCAGCTTGAAGCAACGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
 3099 A 3099  
 1621 A 1621

RESULT 12  
 US-10-352-179-90  
 ; Sequence 90, Application US/10352179  
 ; Publication No. US20040006788A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Guo-liang  
 ; APPLICANT: Liu, Guifu  
 ; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pl  
 ; FILE REFERENCE: 22727/04108  
 ; CURRENT APPLICATION NUMBER: US/10/352,179  
 ; CURRENT FILING DATE: 2003-01-27  
 ; PRIOR APPLICATION NUMBER: 60/352,106  
 ; PRIOR FILING DATE: 2002-01-25  
 ; NUMBER OF SEQ ID NOS: 97  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 90  
 ; LENGTH: 3220  
 ; TYPE: DNA  
 ; ORGANISM: Oryza minuta  
 US-10-352-179-90

Query Match 50.8%; Score 1574.2; DB 6; Length 3220;  
 Best Local Similarity 72.8%; Pred. No. 0;  
 Matches 2168; Conservative 0; Mismatches 763; Indels 46; Gaps 9;

QY 1 ATGCGGAGAGCGGTGCTGAGCATGGCGAGTGGCTGGTGGGCGAGCGCCATCAGCAAGGCC 60  
 DB 1 ATGCGGAGATACAGTACTCAGCATTTGCAAGTCCCTGGTGGGAGTGTGTTAAGCAAGTT 60  
 QY 61 GCCTCCGCTGCTGCGAGCAGCAGCCCTCTGCTGGGCTGCGAAGAGCATCTGCTAT 120  
 DB 61 GCTTCGCTGCTGCGAGCAGCAGCATCTGCTGCTGGGAGTGCAGAGGAGATGCTTC 120  
 QY 121 ATCAAGATGAGCTTAAAGACGATGCAAGCATTTCTTAGAGTGTGCTGAACCTTATGAAAG 180  
 DB 121 ATCAAGATGAGCTTAAAGACGATGCAAGCATTTCTTAGATTTGCTGCGGAA---GCATCAAG 177  
 QY 181 AAGATGACATTAAGGTTTGGCAGAGCAATACGTGACCTGCTCATATGACATGAA 240  
 DB 178 AAGATGACATTAAGGTTTGGCAGAGCAATACGTGACCTGCTCATATGACATGAA 237  
 QY 241 GATTCCTTGCATTAAGTTCATATTTGAAGCCAAACCTTATTTCTGCTGCTGCTG 300  
 DB 238 GATTCCTTGCATTAAGTTCATATTTGAAGCCAAACCTTATTTCTGCTGCTGCTG 297  
 QY 301 AAATCAGAGAACGCCACCGAATGCTATTCGATTCACACCTTAATTAAGATGAA 360



1438 ATCAACCGAAGTATGATTCAAGATCAAGAGTGGSCATAGCAGGAAAAATTAAGACTGCT 1497  
1435 ATCAACCGTATGATGATTCAAGCATCAAGAGCGGATATCAAGGAGGATTTTAAAGACTGT 1494  
1498 CGAATTCATGATATCATCCGTGATATCAAGTTCATCTCGAGACAGGAAAAATTTGTA 1557  
1495 CGAGTCCACGACATCATGCGTGATATTAATAATTTTCAATTTTCTAGAGAGAAAAATTTCA 1554  
1558 TTATTAACCAATGGGAGATGGCTCTGATTTAGTTTCAAGGAAACACTGCCACATAGCATTC 1617  
1555 CTCTTACCGATGGCACTGACTATGATAGTATCATGGAACACTCGGCACATAGAAATTT 1614  
1618 CATGGAGATATGTCCTGC---AAAACTGGAATGGATTTGGAGCATTTATTCGATCATTTAGCT 1674  
1615 CACGGAGTAAGTATTTGCTCTGAAACAAGCTTTGGAGTGGAGCATTTATACGGTCAATTAAC 1674  
1675 ATTTTGGTGACACAGCCCAAGAGTCTAGCACATGCAATTTGTCAGATCAATTAATGAGGATG 1734  
1675 ATGTTTGGTGAGAGGTCCTAGAACCTAGAGCAATTCAGTTTGTTCATCTCAGTTGAGGATG 1734  
1735 TTACGGGTCTTGGAATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACCGT 1794  
1735 TTACGGGTCTTGGAATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACCGT 1794  
1795 ATGTCATTTGTTGGCCTTGAATCACTTGAATCACTTGAATCACTTGAATCACTTGAATCACT 1844  
1795 ATAGTCTCTTGTGCGCACTTGAATCACTTGAATCACTTGAATCACTTGAATCACTTGAATCA 1854  
1845 CATATATTTCACTTTCCAGATCCATTTGGTAACTACAGGGCTTCAAACTTTGAAACATGCC 1904  
1855 TATTTATTTCACTTTCCAGATCCATTTGGTAACTACAGGGCTTCAAACTTTGAAACATGCC 1914  
1905 GAGCACAATCTGAGCACTACCAAGTGAATCAGTAACTCAATGTCGTCATCTCT 1964  
1915 TCAGAGTATATTTCAAGCACTCCCACTCAGATTAATCACTTGAATCACTTGAATCACTTGA 1973  
1965 TCGTTGTATAGGACAGTTTCATTTATGACAACTTTAGTCTAAACCACTTGAATCACTTGAAT 2024  
1974 TCGATGATGATGAAATATTTTCTTCTCTTT-----AACACATATTT 2018  
2025 AACTACACATATGCTGCTTAAAGTATTCACACTTTAGTCTTGTAGTTCGATATGATGCTG 2084  
2019 AACTACACATATGCTGCTTAAAGTATTCACACTTTAGTCTTGTAGTTCGATATGATGCTG 2078  
2085 AAAACAAATTTGCTGAAATGCAATGCGCCACCAAAAGTTTGTGCTGAAATCAATCGGTTG 2144  
2079 TGAACAAATTTGCTGAAATGCAATGCGCCACCAAAAGTTTGTGCTGAAATCAATCGGTTG 2138  
2145 GAAGGTACCCAAAGGAATAGGT-----AAGTTGCGAGACTTGCAGGTTCTAGATATGATG 2200  
2139 CAAGGTACCCAAAGGAATATGTAATAAAACCTCGACTTCAAAATATTTGGAGTATGCTG 2198  
2201 ATATCAGGCGGACAGTATGAGCAATCAAGAGCTGGGCGAGTTAAGCAAGCTGAGGA 2260  
2199 ATATTAGAGGACTAGCACTAGAGCAATCAAGAGTTGGGCGAGTTAAGCAAGCTGAGGA 2258  
2261 AATTAGGTGACAAACAAAGGCTGCAAAAGGAAATGTAAGTACTTTATGACGCA 2320  
2259 AATTATGTTGGTAAACAAAGGATCCAAAGGAAATGTAAGTACTTTATGACGCA 2318  
2321 TTGAGAGCTCTCTTCCCTCAATCTCTCAATGTCGTCGTCGAGGAACTCTCAGATGTTG 2380  
2319 TCCAGAGCTCTCTTCCCTCAATCTCTCAATGTCGTCGTCGAGGAACTCTCAGATGTTG 2378  
2381 GAACATTTAGTGGCTTAGATTTCTATTTCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2440  
2379 GAACATTTAGTGGCTTAGATTTCTATTTCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2438  
2441 TGGATGGAATTTTGGAGGATGCTTAACTGATTTGAGGAGCTCACTCACTCACTCACTCACT 2500  
2439 TGAATGGAATTTTGGAGGATGCTTAACTGATTTGAGGAGCTCACTCACTCACTCACTCACT 2498

2501 TCTCTATTATTGAGGAGCAAACTAAAGGAGTAAACCATCTGCTGATATCTTGGGCGACTGC 2560  
2499 TCAACTTATGAGGAGCAAACTAAAGGAGTAAACCATCTGCTGATATCTTGGGCGACTGC 2558  
2561 CCAACTCATGCTGCTTCTTATCGGATGCTTACCTTGGGAGAACTAGTATTCA 2620  
2559 CCAACTCATGCTGCTTCTTATCTTCAATGCTTACCTTGGGAGAACTAGTATTCA 2618  
2621 AAACAGGAGCAATTTCCAAATCTTGAACACATTTGGATTTATGAATTTGGATTCAGTAAAG 2680  
2619 AAATGGAGCAATTTCCAAATCTTGAACATTTTCAATTTTGAAGCACTAAAGAG 2678  
2681 AGATCAGATTTGAGGAGCGGAGCTCACCTGTTTGAAGAAAGATAGAAATTTTCAAGG 2740  
2679 AGATAGATTTGAGGAGCGGAGCTCAATCTTGTGGAAGAAAGATAGAAATTTTCAAGG 2734  
2741 GGTGGAATCTGGGATTTACTGATATTCATCTTCACTTCCAAAGCTCAAGGAGATTTCAATTA 2800  
2735 GGTGGAATCTGGGATTTACTGATATTCATCTTCACTTCCAAAGCTCAAGGAGATTTCAATTA 2794  
2801 GATACGAGATTAAGTGGCTGGCTTGGTCACTGAGGAGGAGGAGTGAACGACACCCAA 2860  
2795 GATACGAGATTAAGTGGCTGGCTTGGTCACTGAGGAGGAGGAGTGAACGACACCCAA 2854  
2861 ATGCGCCCGTGTCTGCTTAATGATGACCGAAGGATTCACGACCTTGGGCGCTGAAGCCG 2920  
2855 ATCAGCCCGTGTCTGCGAATGAGGAGGAGCGAAGTATCAGACCTTGTGTCGACGCG 2914  
2921 AGGATCTTCTATAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2957  
2915 AAGGATCCCTGTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2951

## RESULT 13

US-10-352-179-84  
; Sequence 84, Application US/10352179  
; Publication No. US20040006788A1

; GENERAL INFORMATION:  
; APPLICANT: Wang, Guo-liang

; APPLICANT: Liu, Guifu  
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in P.

; FILE REFERENCE: 22727/04108  
; CURRENT APPLICATION NUMBER: US/10/352,179

; CURRENT FILING DATE: 2003-01-27  
; PRIOR APPLICATION NUMBER: 60/352,106

; PRIOR FILING DATE: 2002-01-25  
; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 84

; LENGTH: 2940  
; TYPE: DNA

; ORGANISM: Oryza minuta  
; FEATURE:

; NAME/KEY: CDS  
; LOCATION: (1)..(2940)

; OTHER INFORMATION:  
US-10-352-179-84

Query Match 50.4%; Score 1562.2; DB 6; Length 2940;

Best Local Similarity 71.7%; Pred. No. 0;

Matches 2092; Conservative 0; Mismatches 818; Indels 9; Gaps 3;

QY 1 ATGGCGGAGACGGTCTGCTGAGCATGCGAGGTCGCTGCTGGGCGAGCGCCATCAGCAAGGCC 60  
DB 1 ATGGCGGAGACGGTCTGCTGAGCATGCGAGGTCGCTGCTGGGCGAGCGCCATCAGCAAGGCC 60  
QY 61 GCCTCCGCTGCTGCGAGACGACGCTCTCTGCTGGGCGCTCGAGAAAGACATCTGGTAT 120  
DB 61 GCCTCCGCGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
QY 121 ATCAAGAGTGAAGTAAAGCAATGCAAGCAATCTCTTAGAGCTGCTGAATCTTATGAAAAG 180  
DB 121 ATCAAGAGTGAAGTAAAGCAATGCAAGCAATCTCTTAGAGCTGCTGAATCTTATGAAAAG 180

QY	181	AAAGATGAACTATTAAAGGTTTGGCGAGACCAATAAGTACCTGTCTCATATGACATTGAA	240
DB	181	AAAGATGAACTATTAAAGGTTTGGCGAGACCAATAAGTACCTGTCTCATATGACATTGAA	240
QY	241	GATTCCCTTGATGAATTTAGTGCCTATATTGAAGCCAAACCCCTATTTCGTTCAGTTCGGT	300
DB	241	GATTCCCTTGATGAATTTAGTGCCTATATTGAAGCCAAACCCCTATTTCGTTCAGTTCGGT	300
QY	301	AAACTCAGAGAACGCCACCGAATTGCTATCCGTCATCCCAACTTTAAATCAAGAGTTGAA	360
DB	301	AAGCTTGGTGAACGCCATCGAATTGCTGTACAGATTCTCAACTTAAATCAAGAAATTGAA	360
QY	361	GAAGTGACTAGCAGGAACACACGCTACAGTTTGTAGTCMAAGCCTATTTCCTCTGG---	417
DB	361	GAAGTGAGCAACAGGAATACACGCTACAGCTTAAATCAAGCTCAITTTCTCTATAACCA	420
QY	418	GAGATTGATCGAATTCCTATGACAGAAGACATTCGTAATCAGTCAGCTCGCAATGTGGAT	477
DB	421	GAGGATGAGAGGGATTCTACCTAGAGAATGCTCGCAATCGATCAGGTAGCAACACTGAC	480
QY	478	GAGGCTGAGCTTGTGGTGTTCGTACTCCAAGAAAGGCTGCTTGAATCATCGATAC	537
DB	481	GAGTCAGAACTTGTGGGCTTTGCCAAGACTTAAAGATGAGTTGCTTAAACTGATAGATGC	540
QY	538	AATGCTAATGATGTGTCGGGCCAAGGTAATCTGTGTTTGGGATGGGTGGTTTAGGCAAG	597
DB	541	AATACTAATGACGGTCCAGCTAAGTGATATGTGTGTTGGAATCGGTGGATTAGGCAAG	600
QY	598	ACAGCTCTTTGCGAGGAAGATCTTTGAAAGCAAGAGACATTTAGGAAGAACTTCCCTTGC	657
DB	601	ACTACCTCTTGAAGGAAGGCATATGAACAACAGGAACACAT--GAAGAACTTCTTCGTGT	657
QY	658	AATGCTTCGGAATTAACAGTGTCAACATCAATTTACAGGATTGAGCTACTTTAAAGATATGATA	717
DB	658	TGTGCTTGGATCACTGTGTCTCAGTCAATTTGACAGGAAGAATTTCTGAACAAATGATC	717
QY	718	CGCAACTTTCTGGCCCGAGTTCTCTGGATCAACTCTTCCAGAAATTCGAAGGAAGGTG	777
DB	718	AGGCAACTTCTGGGTGCTGATTTCAATTAGACAACTCTTGAAGAATTTAGTGAGAAGTTG	777
QY	778	GTGTGTCGAATACATCATCTTCTTGAGTACTCTGATAGAAGAGCTCAAGGAGAAGAGGTAC	837
DB	778	CTCGTGCAAGTCCAGCATCTCGCTGATCACTTGTGTAAGGCTTAAAGGAGAAAGGTAC	837
QY	838	TTTGTGTCTTAGATGATCTATGGATTTTACATGATTGGAATTTGATTAATGAAATTGCA	897
DB	838	TTTGTGTCTTAGATGATCTATGGATTTTACATGATTGGAATTTGATTAATGAAATTGCA	897
QY	898	TTTCTTAAGAAACAATAGAGGGGAGTCGAATAGTAATAACCACTTCGGAATGTTGATCTT	957
DB	898	TTTCCGAGATTAACACAGAGGTAGTCGCATTAATAAACAACGGAGATGCTGGCTTA	957
QY	958	GGGAGAAAGTGGCCACAGCCCTCACTGGGTGTCACACTTGATTTCTTTCGAGATGAACAT	1017
DB	958	GCTGGAAGGTGTACCTCTCTGATCACTTAATTACCACTTGAACCGGTACATATAGATGAT	1017
QY	1018	GCCTAATCAATTCGTACTGAGAAAAACAATAAAAAATCATGAAGACATGGAATCAATAAA	1077
DB	1018	GCTATACACTTGTCTACTAGCAAGACAAACATAGACTTTGAAGACATGMAAATGATGAG	1077
QY	1078	AATATGCAAAAGATGGTTGAACGAAATTTGTAATAAATAGTGTGCTCTACCAATTAGCAATA	1137
DB	1078	GACTTTGGGCAAGATTTACAAAATTTGGTAAAAAGGTGGTGTATTATTAACCGCTGGCTATA	1137
QY	1138	CTTATCAATAGAGGCTGTGCTTGTCAACTTAAACAGGCTCAGAAATGGGAGAAATTCATGAA	1197
DB	1138	CTCACATAGAGGCAATTCCTGCTACTAGAAATTAATGGAATGGGAAATTTTACAGA	1197
QY	1198	CACCTTCTCTCAGAACTAGAAATAAACCCGAAGCCTCGAAGCTTTGAGGAGAAATGGTGACC	1257
DB	1198	GAACTTCTCTCAGAGCTTTGAGCAATTTCAAGCCTTGAAGCCTAGAACCATGAGAGGATGGTGACC	1257

Qy	1258	CTAGGTTACAACGACCTTACGATCCGCAATTTGAAACCAATGCTTTTGTATCTTAAGTATCTTT	1311
Db	1258	CTAAGCTACAATCACTTACCATCTCACTTTAAACCAATGCTTTCTTTTACTTAAGTATTTTC	1317
Qy	1318	CTGAGGATTTTGAATCAAAAGGAATCTGCTAGTAGGTAGATGATGACAGAGGGTTT	1377
Db	1318	CTGAAGATTTTGAATTTCAAAGGGCGCTGGTAGATAGATGATAGCAGAGGGTTT	1377
Qy	1378	GTTAGACCAAGGTTGGGATGACGACTAAGGATGTCGGAGAAAGTTACTTTAAATGACGTA	1437
Db	1378	GTCAGAGCCACAGATGGGGTGAACATGAGGAGATGTTGGAAATAGTGCATTTTAATGAGCTT	1437
Qy	1438	ATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGCATAGCAGGAAAAAATTAAGACTTGT	1497
Db	1438	ATCAACAGAGTCTGATTTAGCCCTCAAAGTTAGTACAGATGGAGTTGTTTAAGAGATGT	1497
Qy	1498	CGAATTCATGATATCATCTCGTGATATCAAGTTTCAATCTCGAGCAGGAAAAATTTTGTA	1557
Db	1498	CGAATCCCATGATATCATCGGTGATATCATAGTTTCAATTTCTAGAGAGAAAAATTTTGTG	1557
Qy	1558	TTATTAACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAAAAACCTCGCCACATAGCATTC	1617
Db	1558	CTGTGACTAGGAGAGAATCACTGTTGTAGCGGAGAGAGCATCCGCATCTAGCATTT	1617
Qy	1618	CATGGGATATGCTCTCGCAAACTGGATTTGGATTTGGAGCATTTTCATCATATAGCTATT	1677
Db	1618	CATGGGAGCAATGCTCAAGATATGCTTTGGAGTGAACCATCTCGCTCAGTAACTTTG	1677
Qy	1678	TTTGGTGACAGACCAAGAGTCTAGCACATGCACTGAGTTTGFCCAGATCAATGAGGATGTA	1737
Db	1678	TTTGGTGACAGACCTCGGGGCGCAACACCTGCACTTTGTTCACCACAATTTAGGATGCTG	1737
Qy	1738	CGGCTCTTGGATCTTTGAGATGTGACATCTCTTAATCACTCAAAAAAGATTTTCGACCGTATT	1797
Db	1738	AGAGTTTGGATCTGGAAGATGCAAAATTCAAATTCACAAATGATATCAGGAATATA	1797
Qy	1798	GCATTTTGTGCCACTTGAATACTTGAGTATTTGGATATTTGTCATCATATATTCACCTT	1857
Db	1798	GGTGTGTTGGCCACATCAATAATTTGAAATTTTGCAGAGCCTCAACTATTTTATACACTT	1857
Qy	1858	CCGAGATCCATTTGGTAAACTACAGGCGTACAAACTTTTGAACATGCCGAGCACATACATT	1917
Db	1858	CCAAGTCCATAGAAAAATTGCAGTCTGTGCAAAATTTTGNACATGAGGGAGGCAAAATC	1917
Qy	1918	GCAGCATCAACAGTGAGATCAGTAAACTCCCAATGTCGCATATCTTCTGTTGTATAGGA	1977
Db	1918	TCAGCACTAAACACTGAGGTGACTTAACTCTCAGAAATCTCCGTAGCTCCGATGCGAGCGG	1977
Qy	1978	CAGTTTCTATATGACAACTTTTAGTCTAA--ACCACCAATGAAGTGATAACTTAACACA	2034
Db	1978	AGGTCAGGTTCTGGTTACTTTTGGATAATAGATATATCCAGGAATGCTTGATGATCACC	2037
Qy	2035	ATATGCTGCTTAAAGTATTCACACCTTTAGTTTGTGCGGATGATCGTGCAAAAACAATTT	2094
Db	2038	ATGTGCTTACCGATGGTTTCTCAACTTCAATTAATTTTCAGTGACCCGTTGTGAAGTTAAT	2097
Qy	2095	GCTGAATTCACATGGCCACCAAAAGTTGCTGCTTGAATCAATCGGTGTGAAGTACCC	2154
Db	2098	CTTGATATGCATGTCATGTTCTACCGTTGGTCTGTATACAAAGGGTGTGAGGGTGCCA	2157
Qy	2155	AAAGGAATAGTATGTTGCGAGACTTGCAGGTTCTAGAGTATGTAGATATCAGCGGACCC	2214
Db	2158	AGAGGAATTCACACCTTAAAGAGTTTACAGATTTAGAAAGTCGTGGACATCAACAGAACT	2217
Qy	2215	AGTAGTAGCAATCAAGAGCTGGGGCGAGTTAAGCAAGCTCAGGAAAAATAGGTGTGACA	2274
Db	2218	AGTAGGAGGCGATGAGAGCTGGGGAGCTAAATTCAGTTTAAGAAAAATTAAGCGTGACA	2277
Qy	2275	ACAAACGGGTGCAAAAGGAAAAATGTAAAGTACTTTATGAGCCATTTGAGAAAGTCTCT	2334
Db	2278	ACAAAGGCGGCCAAAAATAAGAGTATCAGATATTTTGTGCAGCGATTTGAGAAAGTCTCT	2337
Qy	2335	TCCTCTCAATCTCTCAATGTGGATGCTGCGAGGAATCTCAGATGTGTGGAACACTTGTAGTGC	2394



```
1140 TACAATAGGAGCTGTGCTTGCACATTAACAGGTGTCAAGATGGGAGAAATTTCTATGACA 1199
1143 CACAATAGGAGGCAATCTTCTACTAAGAGATAATAGGAGTGGGAGAAATTTTACAGAGA 1202
1200 CTTTCTTTAGAACTAGAAATAAACCAAGCCTGGAAGCTTTTGGAGAGAAATGGTGACCTT 1259
1203 ACTTCTTTAGAGCTTGAAGAGCAATCAAGCTTAGAGCCATGAGGAGATGGTGACCTT 1262
1260 AGGTTCACACACCTACCATCCATTTGAAACATGCTTTTGTATCTAGTATCTTTCC 1319
1263 AAGCTACAACTACCTTACCATCTCATCTTAACCATGCTTTTACCTAAGTATTTTCCC 1322
1320 TGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGTAGATGAGTAGCAGAGGGTTTGT 1379
1323 TGAAGATTTTGAATTTCAAGAGGGGCGCTGTGTAGATAGATAGCAGAGGGTTTGT 1382
1380 TAGACCAAGGTTGGGATAGCACTAAGATGTGCGAGAAAGTTACTTTATGAGCTAAT 1439
1383 CAGAGCCACAGATGGGGTGAAATGAGGATGTGGAATAGTCACTTTAATGAGCTTAT 1442
1440 CAACCGAAGTATGATTCACAGATCAAGAGTGGGCTAGCAGGAAATAATTAAGACTTGTG 1499
1443 CAACAGAGTCTGATTCAGGCCCTCAAAAGTTAGTACAGATGGAGTTGTTAAGAGATGCG 1502
1500 AATTCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGACAGGAAATTTTGTATT 1559
1503 AATCCATGATATCATCGTGTGATATCATAGTTTCAATTTCTAGAGAGGAAATTTTGTGCT 1562
1560 ATTACCAATGGAGTGGCTCTGATTTAGTTAGGAGAAACACTCGCCACATAGCATTTCCA 1619
1563 GTTGACTAGGAGAGATCACTGTTGTAGGAGAGAGCATCGCCCATCTAGCATTTCA 1622
1620 TGGAGTATGTCCTGCAAACTCGATTTGATTTGAGTGGAGCATTTATCGATCATPAGCTATT 1679
1623 TGGAGCAAAATGCTCAAAAGATATGCTTGGAGTGGAAACCATCTGGGCTCAGTAACCTTGT 1682
1680 TGTGACAGACCCAGAGTCTAGCAGATGAGTGTGTCAGAGTCAATTTGAGAGATGTTAAG 1739
1683 TGGCAGACAGCTGTGGGGGAGACACTGCACTTTGTTTCCACCAATTTAGGATGCTGAG 1742
1740 GGTCTTGATCTTGAAGATGTCATCTTTAATCACTCAAAAGATTTGACCGGTATGTC 1799
1743 AGTGTGATCTGGAAGATGCAAAATTCAAATTCACAAATGATATCAGGAATATAGG 1802
1800 ATTGTGTGACCTTGAATATCTGAGTATGATATGATATGCTCATCCATATATCACTTCC 1859
1803 GTTGTGCGCCACATGAATATTTGAATTTTGCAGAGCTCACTATTTATACACTTCC 1862
1860 CAGATCCATTTGTTAACTACAGGGCTTACAACTTTGAAATGCGGAGCACATACATGTC 1919
1863 AAGTCCATAGGAAATTTGAGTGTGCAATTTTGAACATGAGGAGGCAAAATATCTC 1922
1920 AGCACTACAGTACAGATCAATACTCCAATGCTGTCATCTCTGCTGCTATAGGACA 1979
1923 AGCACTACAACTAGGTGATCACTCCAGATCTCCGAGCTCCGATCCGATCCAGAGAG 1982
1980 GTTTCATTTAGCAACTTTTAGTCTAA---ACCACCAATGAAGTGCATACATCAACAAT 2036
1983 GTCTGTTCTGTTACTTTAGCATAATAGATAATCCCAAGGAATGCTTTGATGATCACCAT 2042
2037 ATGCTGCTTAAGTATTTACACTTTAGTTAGTGTGATGATGATGTCGCAAAACAAATTCG 2096
2043 GTGCTTACCGATGTTTCTTAATCTCAATTAATTTAGTGACCGGTGAAGTTAATTC 2102
2097 TGAATGCAATGCCACCAAAAGTTGCTGCTGATCAATCAATCGGTGTGAAGGTACCCAA 2156
2103 TGAGATATGATGATGATGTTCTACCCGTTGCTGATACAAAGGGTGTGAGGTGCCAAG 2162
2157 AGGATAGTATGATGAGTGTGAGGTTCTGAGTATGATGATGATGATGATGATGATGATGAT 2216
2163 AGGAATTCACCACTAAAGAGTTACAGATTTCTAGAAAGTCTGTTGAGCATCAACAGACTAG 2222
```

## RESULT 15

US-10-656-394A-1  
; Sequence 1, Application US/10656394A  
; Publication No. US20040210957A1

## GENERAL INFORMATION:

; APPLICANT: Wang et al.  
; TITLE OF INVENTION: Cloning and Characterization of the  
; FILE OF INVENTION: broad-spectrum resistance gene P12  
; FILE REFERENCE: 035718/252062  
; CURRENT APPLICATION NUMBER: US/10/656,394A  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2982  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1) ... (2982)  
US-10-656-394A-1

Query Match 50.1%; Score 1553.4; DB 8; Length 2982;  
Best Local Similarity 71.5%; Pred. No. 0;

Matches 2085; Conservative 0; Mismatches 821; Indels 9; Gaps 3;

Qy	3	GGCGGAGACGGTCTGAGCATGCGGAGGTCTGGTGGGCGAGCGCATCAGCAAGGCGC	62
Db	6	GGCGGAGACGGTCTGAGCATGCGGAGGTCTGGTGGGCGAGCGCATCAGCAAGGCGC	65
Qy	63	CTCCGCTGCTGCGGAGCGAGACCGCTCTCTGCTGGGCGTTCGAGAAAGCATCTGGTATAT	122
Db	66	CTCCGCTGCTGCGGAGCGAGACCGCTCTCTGCTGGGCGTTCGAGAAAGCATCTGGTATAT	125
Qy	123	CAAGAGTACGCTAAAGAAACGATCAAGCATCTCTTACAGCTGCTGAACTTATGAAAGAA	182
Db	126	CAAGAGTACGCTAAAGAAACGATCAAGCATCTCTTACAGCTGCTGAACTTATGAAAGAA	185
Qy	183	AGATGAATCTTAAAGTTGGGCGAGAGCAATACGTGACCTGTCATATGATGAA	242
Db	186	AGATGAATCTTAAAGTTGGGCGAGAGCAATACGTGACCTGTCATATGATGAA	245
Qy	243	TTCCCTTGATGAATTTAAGTCCATATTCAGAGCCAAACCTTATTTCTGTCAGTTGGTAA	302
Db	246	TTGCTTACGATTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAG	305
Qy	303	ACTCAGAGACCGCACCGAATCTGATCCGATATCCAACTTCAAACTTAAATCAAGAGTTGA	362
Db	306	GCTTGGTGAACCGCATCGAATCTGATCCGATATCCAACTTCAAACTTAAATCAAGAGTTGA	365
Qy	363	AGTGAAGTACGAGCAACAGCTACAGTTTACGCTTCAAGCTTATTTCTCTGG---CACAGA	419
Db	366	AGTGAAGTACGAGCAACAGCTACAGTTTACGCTTCAAGCTTATTTCTCTGG---CACAGA	425
Qy	420	GATTCAGATGATCTCTATGAGAGCAATCTGTAATCAGTCAGCTCGCAATGTTGGATGA	479
Db	426	GGATGAGAGGATTTCTTACCTACGATGCTCGCAATCGATCAGTACGATCACTGACGA	485
Qy	480	GGCTGAGCTTGTGGGTTTCTGACTCCAGAAAGGCTGCTGAAATGATCGATACCA	539
Db	486	GTCAGAACTTGTGGGCTTTGCGCAAGACTAAAGATGAGTTGCTTTAACTGATAGATGCAA	545
Qy	540	TGCTTAATGATGCTCCGCGCAAGGTAATCTGTGTGTGGGATGGTGGTGGTGGTGGTGGT	599
Db	546	TACTAATGACGGTCCAGCTAAAGTATGATGTGTGTGGTGGTGGTGGTGGTGGTGGTGGT	605
Qy	600	AGCTCTTTCGAGGAGATCTTTGAAAGCGAAGACATATAGGAAGACTTCCCTTCCAA	659
Db	606	TACCCTTTCGAGGAGGATATGAAAGCGAAGACATATAGGAAGACTTCCCTTCCAA	662
Qy	660	TGCTTGGATACAGTGTCAATCTTTCAGAGGATGAGCTTCAAGGATATGATGATGATG	719
Db	663	TGCTTGGATCACTGTGTCTCAGTCACTTTCAGAGGATGAGCTTCAAGGATATGATGATG	722
Qy	720	CCAACTTCTGGGCGGCTCTCTGGATCACTCTTGCAGAGATTCGAGGAGGTTGGT	779
Db	723	GCAACTTCTGGGCGGCTCTCTGGATCACTTTCAGAGGATGAGCTTCAAGGATATGATG	782
Qy	780	GGTCAAGTACATCATCTTCTGAGTACCTGATAGAGAGCTTCAAGGAGGAGGATGATCT	839
Db	783	CGTCAAGTCCAGCATCTCTGATCACTTCTGAGGCTTCAAGGAGGAGGATGATCT	842
Qy	840	TGTTGTTCTAGATGATCTATGGATTTTATGATTTGAAATGGAATGGAATGGAATGGA	899
Db	843	TGTTGTTCTAGATGATCTATGGATTTTATGATTTGGAATGGAATGGAATGGAATGGA	902
Qy	900	TCCTTGAAGAAATTAAGAGGCGAGTCAATAGTAATTAACCACTCGGATGTTGATCTTGC	959
Db	903	TCCTTGAAGAAATTAAGAGGCGAGTCAATAGTAATTAACCACTCGGATGTTGATCTTGC	962
Qy	960	GGAGAGTGTGCGACAGCTCTACTGGTGTACCACTTGTGATTTCTTTCGAGATGAGACGATG	1019
Db	963	TGGAAGGTGTACCTCTGAATCACTTATTTACCACTTGAACCGGTTTACATATAGATGATG	1022
Qy	1020	CATAACATTTGCTAGAGAAACAAATAAAATCATGAGACATGGAATCAATAAATAA	1079
Db	1023	TATACATTTGCTACTAGCAAGACAAATATAGATTTGAGACATGGAATATGATGAGGA	1082

Qy	1080	TATGCAAAAGATGGTTTGAACGAATTTAAATAAATGTGGTGGTCTTACCATTAGCAATACT	1139
Db	1083	CTTGGGCGAGCATAGTTTACAAAATTTGGTGAAGAGGTGGTGGTGGTGGTGGTGGTGGTGGT	1142
Qy	1140	TACATAGAGCTGTGCTTGGCAACTTAAACACAGGTGCTGAATGGGAGAAATTTCTATGAACA	1199
Db	1143	CACATAGAGGAGGATTTCTTGTCTACTTAAAGATTAATGGAGTGGGAGAAATTTTACAGAGA	1202
Qy	1200	CTTCTCTTCAAGAACTAGAAATAAACCCAAAGCTGCGAAGCTTTTGGAGGAAATGGTGACCT	1259
Db	1203	ACTTCTCTTCAAGAACTAGAGCAATCCAAAGCTTGAAGCCATAGAGGAGTGGTGACCT	1262
Qy	1260	AGGTACACACCTTACCATCTTCAATTTGAAACCATGCTTTTGTATCTTATGATCTTTCC	1319
Db	1263	AACTCAATCACTTACCATCTTCAATTTGAAACCATGCTTTTACCTTATGATTTTCCC	1322
Qy	1320	TGAGGATTTTGAATCAAAAGCAATCTCTAGTAGGTAGATGGATAGGATAGGATAGGATAGG	1379
Db	1323	TGAAGATTTTGAATTTCAAGAGGCGCTCTGTAGATAGATAGGATAGGATAGGATAGG	1382
Qy	1380	TAGACCAAGGTTGGATGACGACTAAGATGTGCGAGAAAGTTACTTTTATGAGCTAAT	1439
Db	1383	CAGAGCCACAGATGGGGTGAACATTTGAGGATGTTTGAATAATGATCACTTTTATGAGCTTAT	1442
Qy	1440	CAACCGAAGTATGATTTCAACGATCAAGAGTGGGCTAGCAGCAAAATTTAAGACTTCTCG	1499
Db	1443	CAACAGAGTCTGATTTCAAGGCTTCAAAAGTTAGTACAGATGGAGTTGTTAAGAGATCTCG	1502
Qy	1500	AATTCATGATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGAGAAATTTTGTATT	1559
Db	1503	AATCCATGATATCATCGGTGATATCATAGTTTCAATTTCTAGAGAGGAAATTTTGTGCT	1562
Qy	1560	ATTACCAATGGGAGATGGCTCTGATTTAGTTTCAAGAAACACTCGCACAATAGCATTTCCA	1619
Db	1563	GTTGACTAGGAGAGATCACTGTTGTAGCGGAGGAGCATCGCCCATCTAGCATTTCA	1622
Qy	1620	TGGAGTATGTCTGCAAACTTGGATTTGGATTTGGAGCATTTATCGATCATTTAGCTATTTT	1679
Db	1623	TGGAGCAAAATGCTCAAGATATGCTTGGAGTGGAAACCATCTCGGCTCAGTAATTTGTT	1682
Qy	1680	TGTTGACAGACCCAGAGCTAGACATGCTGATTTTTCAGATCAATTTAGGAGTGTTCAG	1739
Db	1683	TGGGACAGACCTTGTGGGCGGAACTCTGCTTTTTCACCAATTTAGGATGCTGAG	1742
Qy	1740	GCTCTTGGATTTGAGATGTCACATCTTAACTCACTCAAAAGATTTTCGACCGTATTCG	1799
Db	1743	AGTGTGGATCTGGAAGATGCAAAATTTCAAAATTCACAAATGATATCAGAAATATAGG	1802
Qy	1800	ATTGTTGGCTTGAATATCTTGAATTTGGATTTTGGTCACTTCCATATTTTACCTTCC	1859
Db	1803	GTTGTTGGCGCACATGAATATTTGAATTTTGGAGGCTTCACTATTTATACACTTCC	1862
Qy	1860	CAGATCAATTTGGTAAATCTACAGGCGCTTCAAACTTTGAACATGCCGAGCAATACATTCG	1919
Db	1863	AGGTCCATAGGAAATTTGACGTGCTGCAATTTTGAACATGATAGGAGGCAAAATATCTC	1922
Qy	1920	AGCACTACCAAGTGAATCAGTAAATCTCAATGTCATCTCTTCTGTTGATAGGACA	1979
Db	1923	AGCACTAACCACTGAGGTGACTTAAATCTCAGAACTCTCGTAGCTTCCGATGCGAGGAG	1982
Qy	1980	GTTTCAATATGACCACTTTTGTCTTAA---ACCACCAATGAAGTGCATACTAACCAAT	2036
Db	1983	GTCTGTTCTTGTGTTTCTTGTAGCAATATAGATAATCCCAAGGATGCTTGTATGATCACC	2042
Qy	2037	ATGCTGCTTAAAGTATTTCACTTTTGTAGTGGGATGATGCTGCAAAACAAATTTGC	2096
Db	2043	GTCTTACCGATGGTTTCTTAACTTCAATTAATTTTCACTGACCGTGTGAGTTTATTC	2102
Qy	2097	TGAATTTGACATGGCCCAACAAAGTTTGTGGTCTGGAATCAATCGGTGTGAGGTGACCAA	2156
Db	2103	TGAGATATGATGCTGATGTTCTTACCCGTTGCTGCTGATACAAAGGTTGTGAGGTGCCAG	2162





GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 21:31:07 ; Search time 895 Seconds  
(without alignments)  
7989.177 Million cell updates/sec

Title: US-10-656-394A-7

Perfect score: 3099

Sequence: 1 atggcgagacggtgctgag.....scacagctcaagctggtga 3099

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:

- 1: /cgn2\_6/prodata/1/pubna/US08 NEW PUB.seq.\*
- 2: /cgn2\_6/prodata/1/pubna/US06 NEW PUB.seq.\*
- 3: /cgn2\_6/prodata/1/pubna/US07 NEW PUB.seq.\*
- 4: /cgn2\_6/prodata/1/pubna/PCT NEW PUB.seq.\*
- 5: /cgn2\_6/prodata/1/pubna/US05 NEW PUB.seq.\*
- 6: /cgn2\_6/prodata/1/pubna/US03 NEW PUB.seq.\*
- 7: /cgn2\_6/prodata/1/pubna/US10 NEW PUB.seq.\*
- 8: /cgn2\_6/prodata/1/pubna/US11 NEW PUB.seq.\*
- 9: /cgn2\_6/prodata/1/pubna/US11 NEW PUB.seq.\*
- 10: /cgn2\_6/prodata/1/pubna/US11 NEW PUB.seq.\*
- 11: /cgn2\_6/prodata/1/pubna/US11 NEW PUB.seq.\*
- 12: /cgn2\_6/prodata/1/pubna/US11 NEW PUB.seq.\*
- 13: /cgn2\_6/prodata/1/pubna/US60 NEW PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107.8	3.5	2151	9 US-11-031-206-125	Sequence 125, App
2	80.6	2.6	644	9 US-11-031-206-107	Sequence 107, App
3	79.8	2.6	1944	9 US-11-031-206-109	Sequence 109, App
4	79	2.5	1902	9 US-11-031-206-137	Sequence 137, App
5	75.2	2.4	1861	9 US-11-031-206-115	Sequence 115, App
6	67.8	2.2	306	9 US-11-031-206-123	Sequence 123, App
7	49.6	1.6	813	9 US-11-031-206-127	Sequence 127, App
8	48	1.5	634	9 US-11-031-206-139	Sequence 139, App
9	43	1.4	590	9 US-11-031-206-135	Sequence 135, App
10	41	1.3	879	6 US-09-925-065A-284566	Sequence 284566, App
11	40.8	1.3	507	9 US-11-031-206-117	Sequence 117, App
12	40.6	1.3	469	6 US-09-925-065A-284567	Sequence 284567, App
13	40.6	1.3	469	6 US-09-925-065A-284568	Sequence 284568, App
14	40.2	1.3	625	6 US-09-925-065A-107964	Sequence 107964, App
15	40.2	1.3	625	6 US-09-925-065A-107965	Sequence 107965, App
16	39.8	1.3	625	6 US-09-925-065A-107966	Sequence 107966, App
17	39.6	1.3	1103	6 US-09-925-065A-81285	Sequence 81285, A
18	39.4	1.3	563	6 US-09-925-065A-287089	Sequence 287089, A
19	39.4	1.3	20945	8 US-10-995-561-13463	Sequence 13463, A
20	39.4	1.3	23082	8 US-10-995-561-13457	Sequence 13457, A

21	39	1.3	563	6 US-09-925-065A-287087	Sequence 287087, App
22	39	1.3	563	6 US-09-925-065A-287088	Sequence 287088, App
23	38.8	1.3	540	6 US-09-925-065A-794000	Sequence 794000, App
24	38.8	1.3	601	6 US-09-925-065A-814272	Sequence 814272, App
25	38.8	1.3	605	6 US-09-925-065A-810341	Sequence 810341, App
26	38.4	1.2	601	6 US-09-925-065A-736743	Sequence 736743, App
27	38.4	1.2	605	6 US-09-925-065A-730236	Sequence 730236, App
28	38.4	1.2	2310	6 US-09-925-065A-686675	Sequence 686675, App
29	38.2	1.2	208765	7 US-10-330-773-407	Sequence 407, App
30	38	1.2	619	6 US-09-925-065A-511863	Sequence 511863, App
31	38	1.2	622	6 US-09-925-065A-105078	Sequence 105078, App
32	37.6	1.2	540	6 US-09-925-065A-850087	Sequence 850087, App
33	37.6	1.2	627	6 US-09-925-065A-761303	Sequence 761303, App
34	37.6	1.2	633	6 US-09-925-065A-811922	Sequence 811922, App
35	37.6	1.2	1041	6 US-09-925-065A-723466	Sequence 723466, App
36	37.6	1.2	1041	6 US-09-925-065A-723467	Sequence 723467, App
37	37.4	1.2	524	6 US-09-925-065A-148152	Sequence 148152, App
38	37.4	1.2	524	6 US-09-925-065A-148153	Sequence 148153, App
39	37.2	1.2	562	6 US-09-925-065A-424975	Sequence 424975, App
40	37.2	1.2	607	6 US-09-925-065A-381464	Sequence 381464, App
41	37	1.2	2723	6 US-09-925-065A-69776	Sequence 69776, A
42	37	1.2	2723	6 US-09-925-065A-69777	Sequence 69777, A
43	37	1.2	4777	12 US-11-136-327-218	Sequence 218, App
44	36.8	1.2	547	6 US-09-925-065A-314610	Sequence 314610, App
45	36.8	1.2	573	6 US-09-925-065A-380787	Sequence 380787, App

## ALIGNMENTS

### RESULT 1

US-11-031-206-125  
; Sequence 125, Application US/11031206  
; Publication No. US20060031959A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Odell, Joan T.  
; APPLICANT: Meyers, Blake  
; APPLICANT: Thorpe, Catherine  
; APPLICANT: Weng, Zude  
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
; FILE REFERENCE: BB1357 US NA  
; CURRENT FILING DATE: 2005-01-07  
; PRIOR FILING DATE: 2005-01-07  
; PRIOR APPLICATION NUMBER: US/09/566,394  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/133038  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133042  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133427  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133437  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133428  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133438  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133436  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/137667  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 208  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 125  
; LENGTH: 2151  
; TYPE: DNA  
; ORGANISM: Glycine max

US-11-031-206-125

```

Query Match          3.58; Score 107.8; DB 9; Length 2151;
Best Local Similarity 48.14; Pred. No. 5.7e-18;
Matches 415; Conservative 0; Mismatches 427; Indels 21; Gaps 3;

QY 558 CAAGTAAATCTGTGTTCTGGATGGTGTGTTAGGCAAGACAGCTCTTTCGAGGAAGAT 617
DB 1301 CACCATCATCTTTGTGTAGGATGGAGGGCTAGGAAACAACTGTTGCGGAAGAGT 1360
QY 618 CTTTGAAGCGAAGACAGCATTTAGGAAGAACTTCCTTGGCAATGCTTGGATTACAGTGC 677
DB 1361 CTTCAATACCAAGAGTGATTT---GCRACACTTTGATTTGCCATGATGATGATGATGATG 1417
QY 678 ACAATCATTTTACAGGATTCAGCTACTTAAAGATATGATACGCCAACTTCTTGGCCCCAG 737
DB 1418 TCAATCTTCACTGTGGAAGGTTGCTAAGAGACTTGTGAAGAGTTATGCAAGAA 1477
QY 738 TTCTCTGGATCACTTTTGAAGAAATGCAAGGAGGTGTTGGTGGAGTACATCATCT 797
DB 1478 GAAGGTGGATCTCTCT-----CATGATATTTCTGAAATGAAATCGAGATTCAC 1525
QY 798 TTCTGAGTACCTGATAGAGAGCTCAAGGAGAGAGTACTTTTGTGTTCTAGATGATCT 857
DB 1526 GATTGATGAAGTGAAGGCCATTTGCAACGAAGAGGTATGTTGTCATTTTGTATGATG 1585
QY 858 ATGAATTTTCAATGATTTGGAATTTGGAATTAATGAATTTGATTTCTTAAGACATAGAA 917
DB 1586 ATGAGTGTAGAACTTTGGGGTCAAAATTCGAAATTCGATGCTTGTATCTATAAAGTTG 1645
QY 918 GGGCAGTCGAATAGTATTAACCACTCGGAATGTTGATCTTGGCGAGAGTGTGCCACAGC 977
DB 1646 TAGATATTAATCACTAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1705
QY 978 CTCACTGGGTACCACTTGTGATTTCTGAGATGAAGATGATGATGATGATGATGATGATG 1037
DB 1706 GGATAAGGTGATGAAGTGAACCTTTTGACTCAAGAGAAATCTATGCAACTCTTTTGC 1765
QY 1038 AAAAAAATAAATAATCATCAAGACATGAAATCAATAAATAATGCAAAAGATGGTTGA 1097
DB 1766 GAAGGCATACCGATACCAATTAATGGGCAATGTCAGAGATCTTAAGAAATTTCTTC 1825
QY 1098 ACGAATTTAAATAATGTTGGTCTTACATTAAGATGATGATGATGATGATGATGATGATG 1157
DB 1826 TGACTTTGTTGAAAAATGTAAGGGTTTACCATTGGCAATTTGGCTATTTGGTATGCTTT 1885
QY 1158 TGCACTAAACAGGTG-----TCAGATGGGAGAAATTTATGAAACACCTTCTCTCAGA 1211
DB 1886 ATCTGGCAAGAAAGACTCCATTTGATGGGAAATAATAGGCGAGCCTAAGTTCAGA 1945
QY 1212 ACTAGAATAAACCAAGCCTGGAAGCTTTGAGGAGATGTTGACCCCTAGGTACAAACCA 1271
DB 1946 GATGAACAAAAGTCCCATTTAATTTGGCATACAAAGATTTTAGGTTTCAGTTATGATGA 2005
QY 1272 CCTACCATCCATTTGAAACCATGTTTGTGATCTAAGTATCTTTCTGAGGATTTTGA 1331
DB 2006 TTTGCCATTAATCTGAATCAATGCTTATTTGTTGATATCCGAGACTATGA 2065
QY 1332 AATCAAAAGGAATCGTCTAGTAGGTAGATGATGATGATGATGATGATGATGATGATGATG 1391
DB 2066 AGTTAACTCAAAAAGATTAATTTGGCAATGGATGATGATGATGATGATGATGATGATGATG 2125
QY 1392 TGGGATGACGACTAAGATCTCG 1414
DB 2126 AGGAAAACATTAGAGGACCTCG 2148

```

RESULT 2

US-11-031-206-107  
; Sequence 107, Application US/11031206  
; Publication No. US20060031959A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni

```

APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Sakai, Hajime
APPLICANT: Famodu, Omolayo O.
APPLICANT: Odell, Joan T.
APPLICANT: Meyers, Blake
APPLICANT: Thorpe, Catherine
APPLICANT: Weng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
FILE REFERENCE: BE1357 US NA
CURRENT APPLICATION NUMBER: US/11/031,206
PRIOR FILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: US/09/566,394
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133428
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/137667
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Microsoft Office 97
SEQ ID NO 107
LENGTH: 644
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (277)
FEATURE:
NAME/KEY: unsure
LOCATION: (415)
FEATURE:
NAME/KEY: unsure
LOCATION: (471)
FEATURE:
NAME/KEY: unsure
LOCATION: (487)
FEATURE:
NAME/KEY: unsure
LOCATION: (495)
FEATURE:
NAME/KEY: unsure
LOCATION: (497)
FEATURE:
NAME/KEY: unsure
LOCATION: (511)
FEATURE:
NAME/KEY: unsure
LOCATION: (585)
FEATURE:
NAME/KEY: unsure
LOCATION: (599)
FEATURE:
NAME/KEY: unsure
LOCATION: (605)
FEATURE:
NAME/KEY: unsure
LOCATION: (610)
FEATURE:
NAME/KEY: unsure
LOCATION: (639)

```



US-11-031-206-107

Query Match 2.6%; Score 80.6; DB 9; Length 644;  
 Best Local Similarity 52.2%; Pred. No. 5.4e-11;  
 Matches 226; Conservative 0; Mismatches 201; Indels 6; Gaps 2;  
 QY 1123 CTACCATAGCAATCTTACATAGGAGCTGTGCTTGAATCAACAGGTGTGATGG 1182  
 DB 1. CTGCGCACTAGCAATTTGATAGTCGCGCAGCTTGTCTCATCTAGACCAAAATA-AAAT 59  
 QY 1183 GAGAAATCTTATGAACACCTTCTTCCAGAACTAGAAATAAAACCCAGCCTGGAGCTTTG 1242  
 DB 60 TTGGAATCAACATACACAGCTTCGGAGTGAGTTGTCAACCAA-----TGATCATGTC 114  
 QY 1243 AGGAGATGTGACCTTAGGTTTACACCACTACATCCCATGTTGAAACCAATGCTTTTGG 1302  
 DB 115 CGAGCAATCTTAAATCTAAAGTACCATGATCTATCTGGAGATCTCAGAAAATGCTTCTTG 174  
 QY 1303 TATCTAAGTATCTTCTGAGGATTTTGAATCAAAAGAAATCGTCTAGTAGGTAGATGG 1362  
 DB 175 TATTGAGCTTGTCTGAGACTACCCATGTACGGGAGCCCTTGTGCGGCTCTGG 234  
 QY 1363 ATACGAGAAGGTTTGTAGACCAAGGTTGGGATGACGACTAAGGATGTGCGGAGAAATG 1422  
 DB 235 GTGCGAGAAGGTTTGTGTGAGTAAAGAAAGAAATACACCAAGAGGAGTGGCTGAGGGA 294  
 QY 1423 TACTTTAATGAGTATCAACGAGTATGATTCAACGATCAAGAGTGGGCATAGCAGGA 1482  
 DB 295 AATCTGGAATGTATGACCCGTAATATGCTTGAAGTTGTAGACTATGATGAGCTTGGC 354  
 QY 1483 AAAATTAGACTTGTGCAATTCATGATATCATCCGTGATATCAAGTTTCAATCTCGAGA 1542  
 DB 355 AGGTTAGCACTTGCAGATGATATCATGAGGACCTGGCACTTTGTGTGTCGCAAA 414  
 QY 1543 CAGGAAATTTTG 1555  
 DB 415 NAAGAGAAGTTTG 427

RESULT 3

US-11-031-206-109  
 ; Sequence 109, Application US/11031206  
 ; Publication No. US20060031959A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rafalski, Antoni  
 ; APPLICANT: Miao, Guo-Hua  
 ; APPLICANT: Falco, Saverio Carl  
 ; APPLICANT: Sakai, Hajime  
 ; APPLICANT: Famodu, Omolayo O.  
 ; APPLICANT: Odell, Joan T.  
 ; APPLICANT: Meyers, Blake  
 ; APPLICANT: Thorpe, Catherine  
 ; APPLICANT: Weng, Zude  
 ; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
 ; FILE REFERENCE: BB1357 US NA  
 ; CURRENT APPLICATION NUMBER: US/11/031,206  
 ; CURRENT FILING DATE: 2005-01-07  
 ; PRIOR FILING DATE: 2000-05-05  
 ; PRIOR APPLICATION NUMBER: 60/133038  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133042  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133427  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133437  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133428  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133438  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133436

US-11-031-206-107  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/137667  
 ; PRIOR FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 208  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 109  
 ; LENGTH: 1944  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; US-11-031-206-109

Query Match 2.6%; Score 79.8; DB 9; Length 1944;  
 Best Local Similarity 52.2%; Pred. No. 1.6e-10;  
 Matches 227; Conservative 0; Mismatches 202; Indels 6; Gaps 2;  
 QY 1121 GTCTACATAGCAATCTTACATAGGAGCTGTGCTTGAATCAACAGGTGTGATGG 1180  
 DB 12 GCCTGCGCACTAGCAATTTGATAGTCGCGCAGCTTGTCTCATCTAGACCAAAATA-AAC 70  
 QY 1181 GCGAGAAATTTCTATGAACACCTTCTTCCAGAACTAGAAATAAAACCCAGCCTGGAGCTT 1240  
 DB 71 ATTGGAATCAACATACACAGCTTCGGAGTGAGTTGTCAACCAA-----TGATCATG 125  
 QY 1241 TGAGGAGATGTGACCTTAGGTTTACACCACTACATCCCATGTCACGGAAGCCCTTGTGCGGCTCT 1300  
 DB 126 TCCGAGCAATCTTAAATCTTAAGCTACCATGATCTATCTGGAGATCTCAGAAAATGCTTCT 185  
 QY 1301 TGTATCTAAGTATCTTCTGAGGATTTTGAATCAAAAGAAATCGTCTAGTAGGTAGAT 1360  
 DB 186 TGTATGCGAGCTTGTCTTCTGAGACTACCCCATGTCACGGAAGCCCTTGTGCGGCTCT 245  
 QY 1361 GATAGCAGAGGTTTGTAGACCAAGGTTGGATGACGACTTAAGATGTGCGAGAAA 1420  
 DB 246 GCGTCGAGAGGTTTGTCTGAGTAAAGAAAGAAATACACCAAGAGGAGTGGCTGAGG 305  
 QY 1421 GTTACTTTAATGAGCTATCAACCAAGTATGATTCAAGATCAAGAGTGGGCATACGAG 1480  
 DB 306 GAAATCTCATGGAATGTACCCCATGTCACGGAAGCCCTTGTGCGGCTCT 365  
 QY 1481 GAAAAATTAGACTTGTGCAATTCATGATATCATCCGTGATATCAAGTTTCAATCTCGA 1540  
 DB 366 GCAGGTTAGCACTTGCAGATGATATCATGAGGAGGACCTGGCACTTTGTGTGTCGA 425  
 QY 1541 GACAGGAAATTTTG 1555  
 DB 426 AAGAGAAGTTTG 440

RESULT 4

US-11-031-206-137  
 ; Sequence 137, Application US/11031206  
 ; Publication No. US20060031959A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rafalski, Antoni  
 ; APPLICANT: Miao, Guo-Hua  
 ; APPLICANT: Falco, Saverio Carl  
 ; APPLICANT: Sakai, Hajime  
 ; APPLICANT: Famodu, Omolayo O.  
 ; APPLICANT: Odell, Joan T.  
 ; APPLICANT: Meyers, Blake  
 ; APPLICANT: Thorpe, Catherine  
 ; APPLICANT: Weng, Zude  
 ; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
 ; FILE REFERENCE: BB1357 US NA  
 ; CURRENT APPLICATION NUMBER: US/11/031,206  
 ; CURRENT FILING DATE: 2005-01-07  
 ; PRIOR FILING DATE: 2000-05-05  
 ; PRIOR APPLICATION NUMBER: 60/133038  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133042  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133427  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133437  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133428  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133438  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133436

```

; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 137
; LENGTH: 1902
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-11-031-206-137

```

```

RESULT 5
US-11-031-206-115
; Sequence 115, Application US/11031206
; Publication No. US20060031959A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Pamodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; TITLE OF INVENTION: Stress Response

```

```

FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/11/031,206
CURRENT FILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: US/09/566,394
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133042
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/133427
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133437
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133428
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133438
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/133436
PRIOR FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: 60/137667
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Microsoft Office 97
SEQ ID NO 115
LENGTH: 1861
TYPE: DNA
ORGANISM: Oryza sativa
US-11-031-206-115

```

RESULT 6  
US-11-031-206-123/c  
; Sequence 123, Application US/11031206



Db 533 ACAAGAGAGATTTTCAGGTGAGAAATGCGCTGCTGATTAGACCTCTGGGTAGATCC 592  
Qy 1102 ATTGTAATAAATGTGCTCTACCAATTAGCAATCTTACAATAGGAGCTGTGCTTGA 1161  
Db 593 ATTGTGAAACTTTGTGGGGTTTACCACTTGCCATTGTTGGTTAGCAGGACTTGTGGCC 652  
Qy 1162 ACTAAACAGGTGTCAGAAATGCGGAGAAATCTATGAACACCTTCTCTCAGAACTAGAAATA 1221  
Db 653 AAGAAGGAGAGTCAACAAGAGAGTGTCT--AAGATCAAGGAGTGTGGGTCTTAA 710  
Qy 1222 AACCAAGCCTGGAAGCTTTGAGGAGAAATGGTGACCTTAGGTTACAACCACTTACCATCC 1281  
Db 711 CACAGGATAAGAATGAGTAATGATATGCTGAACCTTAGGTATGACAACTGCTCTGAA 770  
Qy 1282 CATTGGAACCATGCTTTTGTATCTAAAGTATCTTTCC 1319  
Db 771 AGATTATGCTTGTCTTTTGTATTTTGAATCTGCTCC 808

RESULT 8

US-11-031-206-139  
; Sequence 139, Application US/11031206  
; Publication No. US20060031959A1

GENERAL INFORMATION:

; APPLICANT: Rafalski, Antoni  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Odell, Joan T.  
; APPLICANT: Meyers, Blake  
; APPLICANT: Thorpe, Catherine  
; APPLICANT: Weng, Zude

; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in

; FILE REFERENCE: BBI357 US NA

; CURRENT APPLICATION NUMBER: US/11/031,206

; CURRENT FILING DATE: 2005-01-07

; PRIOR APPLICATION NUMBER: US/05/566,394

; PRIOR FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: 60/133038

; PRIOR FILING DATE: 1999-05-07

; PRIOR APPLICATION NUMBER: 60/133042

; PRIOR FILING DATE: 1999-05-07

; PRIOR APPLICATION NUMBER: 60/133427

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133437

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133428

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133438

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133436

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/137667

; PRIOR FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 208

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 139

; LENGTH: 634

; TYPE: DNA

; ORGANISM: Triticum aestivum

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (378)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (420)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (456)

; FEATURE:

; NAME/KEY: unsure  
; LOCATION: (495)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (498)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (506)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (546)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (561)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (567)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (577)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (581)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (583)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (599)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (615)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (621)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (623)  
US-11-031-206-139

Query Match

1.5%; Score 48; DB 9; Length 634;

Best Local Similarity 51.1%; Pred. No. 0.026;

Matches 142; Conservative 0; Mismatches 130; Indels 6; Gaps 1;

Qy 1102 ATTGTAATAAATGTGCTCTACCAATTAGCAATCTTACAATAGGAGCTGTGCTTGA 1161

Db 3 ATAGTTGATAGGTGTCTACCTCTACCAATTGTTACCAATTGTTGGTGGCAATGTTGCT 62

Qy 1162 ACTAAACAGGTGTCAGAAATGCGGAGAAATCTATGAACACCTTCTCTCAGAACTAGAAATA 1221

Db 63 TCAAGACAACGATTAGACATTTGGAAATCAAAAATACATCAGCTT-----CGAAGCGAG 116

Qy 1222 AACCCAGGCTCGAAGCTTTGAGGAGAAATGGTGACCCCTAGGTTTACAACCACTTACCATCC 1281

Db 117 TTGTCAAAACAATGATCATGTCCGAGCAATTTTAAACCTGAGCTACCATGACCTTCCAGAC 176

Qy 1282 CATTGAAACCACTGCTTTTGTATCTAAGTATCTTCTCTGAGGATTTGAATCAAAAGG 1341

Db 177 GACCTCAAAACCTGTTTTTATCTAGTCTATTTCTCTGAGGATTTGAATCAAAAGG 1341

Qy 1342 AATCGTCTAGTAGTAGTATGATAGTATGATAGTATGATAGTATGATAGTATGATAGT 1379

Db 237 GAAACCTTGTGCGGCTGTGGGTTGCCGAGGCTTGGT 274

RESULT 9

US-11-031-206-135

; Sequence 135, Application US/11031206

; Publication No. US20060031959A1

; GENERAL INFORMATION:

; APPLICANT: Rafalski, Antoni

; APPLICANT: Miao, Guo-Hua

; APPLICANT: Falco, Saverio Carl

```

: APPLICANT: Sakai, Hajime
: APPLICANT: Famodu, Omolayo O.
: APPLICANT: Odell, Joan T.
: APPLICANT: Meyers, Blake
: APPLICANT: Thorpe, Catherine
: APPLICANT: Weng, Zude
: TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
: TITLE OF INVENTION: Stress Response
: FILE REFERENCE: BBI357 US NA
: CURRENT APPLICATION NUMBER: US/11/031,206
: CURRENT FILING DATE: 2005-01-07
: PRIOR APPLICATION NUMBER: US/09/566,394
: PRIOR FILING DATE: 2000-05-05
: PRIOR APPLICATION NUMBER: 60/133038
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: 60/133042
: PRIOR FILING DATE: 1999-05-07
: PRIOR APPLICATION NUMBER: 60/133427
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/133437
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/133428
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/133438
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/133436
: PRIOR FILING DATE: 1999-05-11
: PRIOR APPLICATION NUMBER: 60/137667
: PRIOR FILING DATE: 1999-06-04
: NUMBER OF SEQ ID NOS: 208
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 135
: LENGTH: 590
: TYPE: DNA
: ORGANISM: Triticum aestivum
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (390)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (423)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (426)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (438)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (468)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (507)..(508)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (514)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (569)
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (582)
: US-11-031-206-135

```

Db	Seq	Score	DB 6	Length	879
64	ACTGGGAAACAAAGAGAGTGGTATCAGGTTGGAAGCTCTATTGTTATGCGCAAGGA	123			
1219	ATAAACCCCAAGCGCTGGAGAGCTTTGAGGAGAAGTGGTGAACCTTAGGTTACAAACCACTACCA	1278			
124	AAAAATCTGACATGTGATGCCATGAATATACATATTATCTTTGAGTTATTTGGAGCTTCCC	183			
1279	TCCCATTTGAACCACTGCTTTTGTATCTAAAGTATCTTTCTTGAGGATTTTGAATCAAA	1338			
184	CATCACCTAGATATGCTCTATTGATTTTGACTATGTTTCTTGAAGATTTATCGGTTGAA	243			
1339	AGG 1341				
244	ATG 246				

RESULT 10  
 US-09-925-065A-284566  
 ; Sequence 284566, Application US/09925065A  
 ; Publication No. US20040181048A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single  
 ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.135  
 ; CURRENT APPLICATION NUMBER: US/09/925, 065A  
 ; CURRENT FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: US 60/243, 096  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252, 147  
 ; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250, 092  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/261, 766  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/289, 846  
 ; PRIOR FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 957086  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 284566  
 ; LENGTH: 879  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-925-065A-284566

Query Match	Best Local Similarity	52.7%	Pred. No. 2.2
Matches	89	Conservative	0; Mismatches 80; Indels 0; Gaps 0;

Qy	Seq	Score	DB 6	Length	879
1001	TCTTGCAGATGAACGATGCGATTAACATCTCTACTGAGAAAAACAAATAAAAAATCATGAAG	1060			
671	TCCGAAATTAAGGAGAGATTAACATCTTAAGGAAATCAATCAGAGATTTGGAAT	730			
1061	ACATGGGAATCAATAAAAAATATGCAAAAGATGGTTGGAACGAATTTGTAATAAATGTGGTC	1120			
731	TGAAAAACTCACATAAAAAAGTTTAAAAATACAAATTTGTAATAAATGTGGTACCTGGACC	790			
1121	GTCTACCAATTAGCAATACCTTACAAATAGGAGCTGTCTTGGCAACTAAACA	1169			
791	AAGCAGATTAAGGAGTTTCAGAGCTTGAACTGATCTTTCAAACTAACA	839			

RESULT 11  
 US-11-031-206-117  
 ; Sequence 117, Application US/11031206  
 ; Publication No. US20060031959A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rafalski, Antoni  
 ; APPLICANT: Miao, Guo-Hua  
 ; APPLICANT: Falco, Saverio Carl  
 ; APPLICANT: Sakai, Hajime  
 ; APPLICANT: Famodu, Omolayo O.  
 ; APPLICANT: Odell, Joan T.





```
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 107964
/ LENGTH: 625
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-925-065A-107964

Query Match      1.3%; Score 40.2; DB 6; Length 625;
Best Local Similarity 49.4%; Pred. No. 3.1;
Matches 131; Conservative 0; Mismatches 133; Indels 1; Gaps 1;

QY      828 GAAGAGTACTTTGTTCTTCTAGATGATCTATGGATTTTACATGATTCGAAATTCGATAAA 887
DB      593 GAGCAGAAAATCTCAATCTCATGTTAAATATGACTCTTGAAAACCTACAAAAGTTCAAGGA 534
QY      888 TGAATTTGCATTTCTTAAGAACAAATAAGAGGGCAGTCGAATAGTAATAACCACTCGGAA 947
DB      533 AGGATATGTAATAGGGAGATACATTTAGAAAAGTAATTTGAAGATAGATTATGAAGCTCCA 474
QY      948 TGTGTATCTTGGCGAGAGTGTGCCACAGCCT-CACTGGTGTCACCACTTCGATTTCTTTC 1006
DB      473 TGTATATCATGCTAAGAGGTTGACATAGATTCCTCATGATTTCCAGTTATATGATTTCC 414
QY      1007 AGATGAACGATGCCATAACATTCCTACTGAGAAAAACAAATAAATCATGAACATGG 1066
DB      413 TCTGGAAGTGGGAAATACCTTTATTGATAATACTAAGTAGAAATATAAATTTAAAAATGG 354
QY      1067 AATCAATAAATAATATGCAAAAGAT 1091
DB      353 AATATATGTTAAATATATATACATGAT 329
```

Search completed: March 9, 2006, 22:25:16  
Job time : 897 secs

```
RESULT 15
US-09-925-065A-107965/c
/ Sequence 107965, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, **FASTA**  
Run on: March 9, 2006, 21:39:16 ; Search time 423 Seconds  
(without alignments)  
4336.746 Million cell updates/sec

Title: US-10-656-394A-8  
Perfect score: 5268  
Sequence: 1 MAETVLSMARSLVGSALSKA.....SQVLTITNDSERIGTAQAG 1032

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues  
Total number of hits satisfying chosen parameters: 2506114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.spool -DBV=xlp  
-Q=/abss/ABSSWEB.spool/US10656394/runat 09032006 094019 648/app query.fasta\_1  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LCOPCL=0  
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss03p -USER=US10656394 @CGN 1.1 290 @runat 09032006 094019 648 -NCPUS=6  
-ICPU=3 -NO MAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1182	22.4	3925	3	US-09-330-330-2
2	975.5	18.5	10322	3	US-09-330-330-3
3	637.5	12.1	5222	3	US-09-336-948B-68
4	637.5	12.1	5222	3	US-09-993-170-57
5	637.5	12.1	5696	3	US-09-993-170-60
6	618	11.7	3099	3	US-09-360-186-2
7	618	11.7	3099	3	US-09-864-680A-2
8	614	11.7	31491	3	US-09-360-186-1
9	614	11.7	31491	3	US-09-864-680A-1

10	609.5	11.6	2718	3	US-09-360-186-4	Sequence 4, Appli
11	609.5	11.6	2718	3	US-09-864-680A-4	Sequence 4, Appli
12	607.5	11.5	4465	3	US-08-930-996A-3	Sequence 3, Appli
13	602	11.4	4208	3	US-09-004-838-1	Sequence 1, Appli
14	594.5	11.3	4163	3	US-09-004-838-70	Sequence 70, Appli
15	580.5	11.0	4946	3	US-08-930-996A-1	Sequence 1, Appli
16	572	10.9	3741	3	US-08-803-286A-1	Sequence 1, Appli
17	564	10.7	5475	2	US-08-680-327-1	Sequence 1, Appli
18	564	10.7	5475	2	US-08-228-246-3	Sequence 3, Appli
19	557	10.6	9870	3	US-09-245-928A-15	Sequence 15, Appli
20	557	10.6	51952	3	US-08-947-823-1	Sequence 1, Appli
21	552	10.5	3997	3	US-08-947-823-2	Sequence 2, Appli
22	549	10.4	3982	3	US-08-947-823-4	Sequence 4, Appli
23	535	10.2	2353	3	US-09-004-838-2	Sequence 2, Appli
24	535	10.2	10968	2	US-08-680-327-2	Sequence 2, Appli
25	535	10.2	10968	2	US-09-228-246-1	Sequence 1, Appli
26	514.5	9.8	5134	2	US-08-310-912A-157	Sequence 157, App
27	514.5	9.8	5134	3	US-09-301-085-157	Sequence 157, App
28	514.5	9.8	5134	6	PCT-US95-04589-157	Sequence 157, App
29	465	8.8	1662	3	US-09-004-838-6	Sequence 6, Appli
30	442	8.4	5113	3	US-09-336-946B-3	Sequence 3, Appli
31	442	8.4	5757	3	US-09-336-946B-1	Sequence 1, Appli
32	442	8.4	5757	3	US-09-993-170-56	Sequence 56, Appli
33	405.5	7.7	2903	2	US-08-310-912A-1	Sequence 1, Appli
34	405.5	7.7	2903	3	US-08-841-089-1	Sequence 1, Appli
35	405.5	7.7	2903	3	US-09-301-085-1	Sequence 1, Appli
36	405.5	7.7	2903	6	PCT-US95-04589-1	Sequence 1, Appli
37	405.5	7.7	2903	6	PCT-US95-04589-1	Sequence 1, Appli
38	378.5	7.2	3432	2	US-08-310-912A-141	Sequence 141, App
39	378.5	7.2	3432	3	US-09-301-085-141	Sequence 141, App
40	378.5	7.2	3432	6	PCT-US95-04589-141	Sequence 141, App
41	362	6.9	4211	3	US-09-004-838-106	Sequence 106, App
42	332	6.3	3756	3	US-09-813-742A-2	Sequence 2, Appli
43	332	6.3	3756	2	US-08-261-663A-2	Sequence 2, Appli
44	332	6.3	3760	3	US-09-357-206A-2	Sequence 2, Appli
45	332	6.3	3760	6	PCT-US95-07754A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-330-330-2

; Sequence 2, Application US/09330330  
; Patent No. 6274789

GENERAL INFORMATION:

APPLICANT: Yano, Masahiro  
APPLICANT: Iwamoto, Masao  
APPLICANT: Katayose, Yuichi  
APPLICANT: Sasaki, Takuji  
APPLICANT: Wang, Zi-Xuan  
APPLICANT: Yamanouchi, Utako  
APPLICANT: Iehimaru, Lisa

TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE

NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/330,330

FILING DATE: 11-JUN-1999

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 10-181455

FILING DATE: 12-JUN-1998

ATTORNEY/AGENT INFORMATION:



1699 CTCCTGAGTGAGAGGATTTGAGGAGGCTACATATTTGGATGATCAGAACATCCAGAG 1758  
Db  
361 MetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeu 380  
Qy  
1759 TTGGTTAAAGAGCAAAACAAATCTTAAAGAGTGCGATGCGCTTGCCTTGCATATGTT 1818  
Db  
381 ThrIleGlyAlaValLeuAlaThr-----LysGlnValSerGluThrPheGluValPheTyr 398  
Qy  
1819 GTCATAGGTGGATTTCTTGCCAAACCGACCAAGAGCCCGAGAGAGTGAGAAATTTGAAC 1878  
Db  
399 GluHisLeuProSerGluLeuGluIleValAsnProSerLeuGluAlaLeuArgMetVal 418  
Qy  
1879 GAGAAATCAATCTGAGTTGGAATGAATCCAGAGCTTGAATGATGAAGACCGTCTT 1938  
Db  
419 ThrLeuGlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIle 438  
Qy  
1939 GAAAAAGCTATGATGTTTACCATCATCTCAAGTCATGTTTTTATATCTGTCCATT 1998  
Db  
439 PheProGluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGly 458  
Qy  
1999 TTCCCTGAAGACCAAGATCATTTAGTCGAAGCGTTTGTGTCATCGTTGGGCAGCAGAGGT 2058  
Db  
459 PheValArgProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGlu 478  
Qy  
2059 TACTCAACTGCAGCACATGGGAAATCTGCCATTGGAATAGCTAACCGCTACTTTCATGGA 2118  
Db  
479 LeuIleAsnArgSerMetIle-----GlnArgSerArgValGlyIleAlaGlyLys 495  
Qy  
2119 CTCAAGATAGAGCAATGATTTTACCATTCAGCAATCA-----GGTAGCAGCAGGAA 2172  
Db  
496 ---IleLysThrCysArgIleHisAspIleIleArgAspIleThrValSerIleSerArg 514  
Qy  
2173 TCAATTGACTTTCGAAAGTCCATCATCTGATGCGTGCATCGCCATCTCAAGTCAAGC 2232  
Db  
515 GlnGluAsnPheValLeuLeuProMetGlyAspGlySerAspLeuValGlnGluAsnThr 534  
Qy  
2233 GAGGAAACCTGTTTTTATAGGTGGAGGAGCTGCAGCGGTACATACATGTCGAATT 2292  
Db  
535 ArgHisIleAla-----PheHisGlySerMetSerCysLysThrGlyLeu--- 549  
Qy  
2293 CGTCATCTGTATAGTAGCACTCGAAGGAGAGATAAGTAGTAATTCGAGGCGCATAGTG 2352  
Db  
550 AspTrpSerIleIleArgSerLeuAlaIlePheGlyAspArgProLysSerLeuAlaHis 569  
Qy  
2353 GACTGTCCGAAATAGATCGTTATCTCTGTTGGGAGTGGAAAGCCATTTTGTGTTAT 2412  
Db  
570 AlaValCysProAspGlnLeuArgMetLeuArgValLeuAspLeuGluAspValThrPhe 589  
Qy  
2413 GGC-----AAGATGAGGTTTATACGAGTGTGCTTGAAGGG---ACTAGA 2457  
Db  
590 LeuIleThrGlnLysAspPheAspArgIleAlaLeuLeuCysHisLeuTyrLeuSer 609  
Qy  
2458 GGTCTAGAAATATCATCCCTGATCAGATTTGGAAGCTTATACCTTAAATAATTCCTTCT 2517  
Db  
610 IleGlyTyrSerSerIleTyrSerLeuProArgSerIleGlyLysLeuGlnGlyLeu 629  
Qy  
2518 CTACAGGATGCTATGTTATGATCTACTGCGAGATTCTGCGCACTTGTGAGCACTC 2577  
Db  
630 GlnThrLeuAsnMetProSerThrTyrIleAlaLeuProSer-----GluIle 646  
Qy  
2578 CAGATGCTAGACATCAGAGGTATCATATGTAAGGCTTTGCGCAAAACCATCATCAAGCTT 2637  
Db  
647 SerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPheHisTyrAspAsnPhe 666  
Qy  
2638 CAGAGCTACAGTACATTCATGCTGGCGCAAAACAGACTATGATGGGAGGAAAGCAT 2697  
Db  
667 SerLeuAsnHisProMetLys-----CysIleThrAsnThrIleCysLeuProLys 683  
Qy  
2698 AGTTTATGTCAGAGGTGTCGTAAGGTGGGATGTATATGTGCAACATGTGCTCCCTCTT 2757  
Db  
684 ValPheThrProLeuValSerArgAspArgAlaLysGlnIleAlaGluLeuHis--- 702  
Qy  
2758 CTT-----TCGGAATGATGATGCTCCCTCTCCATAAG 2787  
Db

703 ---MetalThrLysSerCysTrpSer----- 710  
Qy  
2788 GCCCTAGCCGCGGTGATGCGTGACCTTCGCTTGTGCGGTGAATTCCTCATCTATCATG 2847  
Db  
711 -----GluSerIleGlyValLysValProLysGlyIleGlyLysLeuArgAsp 726  
Qy  
2848 ACGGAGGTACATGAGAGGAGCGCTATGTCGCAAGTGGGATTAAGAACTGAAGAC 2907  
Db  
727 LeuGlnValLeuGluTyrValAlaPheIleArgThrSerSerArgAlaIleLysGluLeu 746  
Qy  
2908 TTGCACACACTAAGCAACATAAATGTCGGAAGG---GGAATGCCATCTCAGAGATATC 2964  
Db  
747 GlyGlnLeuSerLysLeuArgLysLeuGlyValThrThrAsnGlySerThrLysGluLys 766  
Qy  
2965 GGAATGCTCACAGGATTAACAAGTTAGGATGGCT-----GGCATCAACAAGAAGAT 3018  
Db  
767 CysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLeuGlnSerLeuHisValAsp 786  
Qy  
3019 GGACGAGCGTTTCGCTGGCCATTTCAACCTCAACAAGCTGGAATCCTGTGTGAT 3078  
Db  
787 AlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLeuAspSerIleSerSerProPro 806  
Qy  
3079 TCAGCAGGATGCCG-----GGCTTGTGTTGCTTGGATGATATATCTCGCTCCG 3132  
Db  
807 ProLeuLeuArgThrLeuValLeuAspGlyIleLeuGluMetProAsnTrpIleGlu 826  
Qy  
3133 GAAACCTACAGAGCTCAAGCTGTACGCGAGTTTGAACAGCTTGCAGGATGATCAAG 3192  
Db  
827 GlnLeuThrHisLeuLysLeuValIleTyrLeuLeuArgSerLysLeuLysGlu---GlyLys 845  
Qy  
3193 GAGCTCCAGCATCTCGTGAAGTTAAACTAGTAGTACTAGGCTATTTGAGCAGCAGCT 3252  
Db  
846 ThrMetLeuIleLeuLeuValLeuProAsnLeuMetValLeuHisLeuTyrArgAsnAla 865  
Qy  
3253 GCTATGGAATTCCTTGGGAACTACCGAAGTGGAAATCTAGTATT-----TCACCG 3306  
Db  
866 TyrLeuGlyGluLysLeuValPheLys-----ThrGly---AlaPheProAsnLeu 881  
Qy  
3307 TTTAAGAGTGAAGAAATTCATTTCAAGCTCCGAGACTCGGACTGCTTTGTAGCCCTC 3366  
Db  
882 ArgThrLeuTrpIleTyrGluLeuAspGlnLeuArgGluIleArgPheGluAspGlySer 901  
Qy  
3367 AGGTGCTCAAGCTTTCAGGATTTATGGGCATCAATCAGTGAAGTTTGAGGAAGCA 3426  
Db  
902 SerProLeuLeuGluLysIleGluIle---GlyGluCysArgLeuGluSerGlyIleThr 920  
Qy  
3427 ATGCCCAAACTTGAGAGCTCGAGTCCAAAGGCGGAAATAGAAATGGAATTTGCTTCT 3486  
Db  
921 GlyIleIleHisLeuProLysLeuLysGluIleProIleArg-TyrGlySerLysValAl 940  
Qy  
3487 GGTTAGATTTCTCCAAAACATCAACGAAGTCCAGCTCAGTGTGTTGTTCCCGCAT 3546  
Db  
940 aGlyLeuGlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeuMe 960  
Qy  
3547 CATGATAGGA-----TAAGAGCCGCGCGC---CCGCGGCGCTGATTATGAGACT 3594  
Db  
960 tTyrSerAspArgTyrHisAspLeuGlyVala-----GluAl 973  
Qy  
3595 GCTGGGAGAGAGGTACAGGAGCAGGCGCAAGGAGGTGACATGAAGAGGAAATC 3654  
Db  
973 aGluGlySerSerIleGluValGlnThrAlaAspProValProAsp 988  
Qy  
3655 CGAGAACAGCTTGTCTCGGAATCCAAACCAACCCATCATCTACCTGAG 3700  
Db

## RESULT 2

US-09-330-330-3  
; Sequence 3, Application US/09330330  
; Patent No. 6274789  
; GENERAL INFORMATION:  
APPLICANT: Iwamoto, Masahiro  
APPLICANT: Yano, Masahiro  
APPLICANT: Katayose, Yuichi

APPLICANT: Sasaki, Takuji  
 APPLICANT: Wang, Zi-Xuan  
 APPLICANT: Yamanouchi, Utako  
 APPLICANT: Ishimaru, Lisa  
 TITLE OF INVENTION: RICE GENE RESISTANT TO BLAST DISEASE  
 NUMBER OF SEQUENCES: 13  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/330,330  
 FILING DATE: 11-JUN-1999  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP-10-181455  
 FILING DATE: 12-JUN-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Ph.D., J.D., Janis K.  
 REGISTRATION NUMBER: 34,819  
 REFERENCE/DOCKET NUMBER: 06501/032001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10322 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic DNA  
 US-09-330-330-3

Alignment Scores:  
 Pred. No.: 6,54e-99 Length: 10322  
 Score: 975.50 Matches: 319  
 Percent Similarity: 45.2% Conservative: 181  
 Best Local Similarity: 28.9% Mismatches: 372  
 Query Match: 18.5% Indels: 235  
 DB: 3 Gaps: 36

US-10-656-394A-8 (1-1032) x US-09-330-330-3 (1-10322)

163 LeuValGlyPheSerAspSerLysArgLeuLeuMetIleAspThrAsnAlaAsn 182  
 6119 CTTATTGGCGGAGAGAAATAATATCGAAATAACACACTTAATT---TTAAACAATGAT 6175  
 183 AspGlyProAlaIleValIleCysValValGlyMetGlyGlyLeuGlyLysThrAlaLeu 202  
 6176 AGCCAGCAGGTTTCAGGTGATCTCTGTGGGAAATGGTGGCTTGGAAAAACCCACTA 6235  
 203 SerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsnAlaTrp 222  
 6236 GTAAGCGGTGTTTATCAAGCCCAAGG---CTGAGTGATAAGTTTGCACAGTATGTTTT 6292  
 223 IleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArgGlnLeu 242  
 6293 GTCACAAATCATGCGTCCTTTCATCTCTGTAGAGCTCTTAGGAGTTGGCTGAGCACTA 6352  
 243 ---LeuGlyProSerSerLeuAspGlnLeuGln-----GluLeuGlnGly 257  
 6353 CATAAAGGATCTTCTAAGAGGAAGAACTGTAGAAAATAGAGTCAGCAGTAGAAGATCA 6412  
 258 LysValValValGlnValHisHisLeuSerGluTyrlleuIleGluLeuLysGluLys 277  
 6413 CTAGCATCGATGGAGGATACCGAGTTGACTGGCGAGTTGAAAAGCGCTTTTAGAAGAAA 6472  
 278 ArgTyrPheValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGlu 297  
 6473 AGTTGCTTGTGTTCTTAGATGATTTCTCAGATACCTCAGAAATGGGACGATAAACCA 6532  
 298 IleAlaPheProLysAsnAsnLysLysGlySerArgIleValIleThrArgAsnVal 317  
 6533 ACGTTATTCCCTCTG---TTGGAAAGACAGCGCGAATTAATGTGACTACAGAAAGAG 6589  
 318 AspLeuAlaGluLysCysAlaThrAlaSer---LeuValTyrHisLeuAspPheLeuGln 336  
 6590 AATATTGCCAACCATTTGCTCAGCGAAAATGGAAAATGTGCACAACTTAAGTTCTTAA 6649  
 337 MetAsnAspAlaIleThrLeuLeuLeuArgLysThrAsn----- 349  
 6650 CATAATGATGCAATTTGCTGCTTGTAGTGAGAGGT- AATATAAGTGTGCTCCATTTTCT 6708  
 349 ----- 349  
 6709 TCGTTTGTATATCTTTTAATCAATTTGAGTTTCAATCAAGATGATATTGTGTCATGCG 6768  
 349 ----- 349  
 6769 AAATAGCATATCTAGATTCATATACAACTTAATCTGTTCTCACAAATAGCAATGCG 6828  
 349 ----- 349  
 6829 TTCCTAAATGACCTGCGATTGGATGGAGCTTAGATGTGACTTTGTTTGTATGTAATGG 6888  
 349 ----- 349  
 6889 TGGCCTTCATCTTCATTGTTTAAATAGTAAAGAGCTATTCTTAAATTTAATTTTTTGT 6948  
 350 -----LysAsn 351  
 6949 TTACTTTTAGACCAACAATAAGCTTAATTTGATCATCTATGTCAGGTATTTGAGGAGGCTACA 7008  
 352 HisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIleValAsnLys 371  
 7009 TATTGGATGATCAGAAACAATCCAGAGTTGGTTAAAGAGCAAAAACAATCTTAAAGAG 7068  
 372 CysGlyArgLeuProLeuAlaIleLeuThrIleGlyValValLeuAlaThr-----Lys 389  
 7069 TCGATGAGTCCCTTCGCAATAGTTGTTCATAGTGGATTCTTGGCAACCGACCAAG 7128  
 390 GlnValSerGluTrpGluLysPheTyrGluHisLeuProSerGluLeuLeuAsnPro 409  
 7129 ACCCCAGAGAGTGGAGAAAATTTGAACGAGAAATATCAATGCTGAGTTGGAAATGAATCCA 7188

86 PheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuValLysLeuArgGluArg 105  
 5760 TTCAAATAGGATCCAAACTAAGTTTATCTACTAGCTGCAATTAATGAAGGATATAT 5819  
 106 HisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGluGluVal----- 122  
 5820 CATATTGTTGTTGATCTTCTCATGACCG-AAAACAAGGCTAAACACTATCCATGTATGA 5878  
 123 -----SerSerArgAsnThrArgTyrSerLeu----- 131  
 5879 AATTTAAGGCTAAAAGTTGTTCTTAATCATTTGCTCCCTTTGTTAGGGTTCCCAATTT 5938  
 132 -----ValLysProLys----- 136  
 5939 ATAGAGGATTCAGTGAAGCCAGTGTCTATCTCGGATGTGCCCATCAAGATCAACAAT 5998  
 137 -----SerGlyThrGluIleAsp-----MetAspSerTyrAlaGluAsp 149  
 5999 CATACAGTGGCCCATGGTGAGATTATAGATGATCAATCAATGATGCTGATGAGAGAG 6058  
 150 IleArgAsnGlnSerAlaArgAsnVal-----AspGluAlaGlu 162  
 6059 GTGGCTAGAAAGAGTCTTACTCGCATTAGGACAAAGTGTGTTGCTTCCGAGGAATCACA 6118

QY    410 SerLeuGlnAlaLeuAArgMetValThrLeuGlyTyrAsnHisLeuProSerHisLeu 429  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7189 GAGCTTGGAATGATAAGAACCGCTCTTGAAAAAAGCATGATGGTTTTTACCATTACATCTC 7248

QY    430 LysProCysPheLeuTyrLeuSerIlePheProGluAspPheGluIleLysAspAsnArg 449  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7249 AAGTCATGTGTTTATATCTGTCCATTTTCCCCTGAAGACCCAGATCATTAATGTCGAAGCGGT 7308

QY    450 LeuValGlyArgTrpIleAlaGluGlyPheValArgProLysValGlyMetThrThrLys 469  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7309 TTGGTGCATCGTTGGCGAGCAGAAGGTTACTCAATGCCAGCATATGGGAAATCTGCCATT 7368

QY    470 AspValGlyGluSerTyrPheAsnGluLeuIleAsnArgSerMetIle-----Gln 486  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7369 GAATTAGCTAACCGCTACTCTTCATGGAACTCAAGAATAGAACGATGATTTTACCATTCCAG 7428

QY    487 ArgSerArgValGlyIleAlaGlyLys---IleLysThrCysArgIleHisAspIle 505  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7429 CAATCA-----GGTAGCAGCAGGAATCAATTGACTCTCTGCAAAGTCCATGATCTCATG 7482

QY    506 ArgAspIleThrValSerIleSerArgGlnGluAsnPheValLeuLeuProMetGlyAsp 525  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7483 CGTGACATCGGCATCTCAAAAGTCAACGAGGAGAAAACCTTGTTTTTATAGGCTGCAGAAAGGC 7542

QY    526 GlySerAspLeuValGlnGluAsnThrArgHisIleAla-----PheHisGly 541  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7543 TGCAGCGGTACATACATGTGGCAATTCGTGCATCTTGCTCTAATAGTCGCACTGGAAGCGA 7602

QY    542 SerMetSerCysLysThrGlyLeu---AspTrpSerIleIleArgSerLeuAlaIlePhe 560  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7603 GATAAGAGTGAATTCGAGGCGCATAGTGACCTGCCCCGAATACGATCGTTATCTCTGTTT 7662

QY    561 GlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArg 580  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7663 GGGGAATGGAAAGCCATTTTGTATTATGCG-----AAGATGAGGTTTATACGA 7710

QY    581 ValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAla 600  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7711 GTGCTTGACTTTGAAGGG--ACTAGAGGCTAGATATATCATCACCTTGATCAGATTGG 7767

QY    601 LeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuPro 620  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7768 AAGCTTAATACCTTAAATTCCTTCTCTACGAGGATGCTATCGTATTGATCTACTGCCA 7827

QY    621 ArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAla 640  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7828 GATTTACTGGGCAACCTGAGGCACTCCAGATGCTAGACATCAGAGGTACATATGTAAG 7887

QY    641 AlaLeuProSer-----GluIleSerLysLeuGlnCysLeuHisThrLeuArgCys 657  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7888 GCTTTGCCAAAAACCATCATCAAGCTTCAGAACTACAGTACATTCATGCTGGGCGCAAA 7947

QY    658 IleGlyGlnPheHisTyrAspAsnPheSerLeuAsnHisProMetLys-----Cys 674  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
7948 ACAGACTATGATGGAGGAAAACCATGATTTAATGCAGAGGTGCTGAAGTGGATGT 8007

QY    675 IleThrAsnThrIleCysLeuProLysValPheThrProLeuValSerArgAspArg 694  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
8008 ATATGTCAACATGTGCTCCCTCTTCTT-----gluSerIleGlyValLysVal 717

QY    695 AlaLysGlnIleAlaGluLeuHis-----MetAlaThrLysSerCysTrpSer----- 710  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
8038 TCGAAATGATGGCCCTCTCCATAAGCCCTAGCCGGGCTGATCGGTGAACTTTCCT 8097

QY    711 -----gluSerIleGlyValLysVal 717  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
8098 TGCTCGTGAAATTCCTCATCATCAGCGAGTATCATGAAGAGAAAGCGGCTATGTGT 8157

QY    718 ProLysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgArg 737  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:  
8158 CCAAGTGGGATTAGAAAACCTGAAAGACTTCACACACTAAGGACATATATGTCCGAAGG 8217

QY    738 ThrSerSerArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyVal 757  
Db                 :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESIST 3

```

RESUL 3
US-09/336-946B-68
; Sequence 68, Application US/09336946B
; Patent No. 6479731
; GENERAL INFORMATION:
; APPLICANT: Valent, Barbara S.
; APPLICANT: Bryan, Gregory
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: A PI-ta GENE CONFERRING DISEASE RESISTANCE TO PLANTS
; FILE REFERENCE: BB-1136
; CURRENT APPLICATION NUMBER: US/09/336,946B
; CURRENT FILING DATE: 1999-06-21
; PRIOR APPLICATION NUMBER: 60/095229
; PRIOR FILING DATE: 1998-08-04
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 68
; LENGTH: 5222

```



TYPE: DNA  
ORGANISM: Oryza sativa  
US-09-336-946B-68

## Alignment Scores:

Pred. No.: 6,48e-61 Length: 5222  
Score: 637.50 Matches: 256  
Percent Similarity: 40.0% Conservative: 168  
Best Local Similarity: 24.2% Mismatches: 381  
Query Match: 12.1% Indels: 255  
DB: 3 Gaps: 35

US-10-656-394A-8 (1-1032) x US-09-336-946B-68 (1-5222)

Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20  
Db 2426 ATGGCGCGCGGTCATTCATCGCAGGCGTTCATCATCGCGTCCCTGACGAGCAGCTC 2485  
Qy 21 AlaSer-----AlaAlaAlaAspGluThrSerLeuLeu 31  
Db 2486 GACTCGCTGCTGTCAGCGCGCGGAGCGCGCGCTGCGCAACGCTGCTCGCTCGCG 2545  
Qy 32 LeuGlyValGluLysAspIleThrPyrIleLysAspGluLeuLysThrMet-----Gln 49  
Db 2546 AAGGGGAG 2605  
Qy 50 AlaPheLeuArgAla-----AlaGluLeuMetLysLysAspGluLeuLeuLys 66  
Db 2606 TACTACCTCTGTCGAGCGCGCGTCAGACCGCGCGCCAGCGCTCGACCGCGCGG 2665  
Qy 67 ValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGluAspSerLeuAspGluPhe 86  
Db 2666 TGCTGGGCTAAGGAGGTTCGCGAGTCTCTACGACGTCGACGACTTCTTCGACGAGCTA 2725  
Qy 87 LysValHisIle----- 90  
Db 2726 ACGACCCAGCTCTCCACACCGCGCGCGCGCGATGCGAGTAGCAGTGTGTCGCAAG 2785  
Qy 91 -----GluSerGlnThrLeuPheArgGlnLeuValLysLeuArgGluArgHisArgIle 108  
Db 2786 AAGATGATCAGCAGCATGATCGCGCGCTTCGAGGGGAGCTTAACCGCGCGCGTGGATC 2845  
Qy 109 AlaIleArgIleHisAsnLeuLysSerArgValGluGluValSerSerArgAsnThrArg 128  
Db 2846 GCGCAGGAGTCACTGTTGAGGCGCGCGTGAAGAGGAGCATTCGCCGCCACGAGAGC 2905  
Qy 129 TyrSerLeuValLysProIleSerGlyThrGluIleAspMetAspSerTyrAlaGlu 148  
Db 2906 TACCATCTTGGCAGGCGCACCTCGAGCTCGAGCGCGAGGAGAGAGAGAGAGAGAGAG 2959  
Qy 149 AspIleArgAsnGlnSerAlaArgAsn----- 157  
Db 2960 GACGATCGCGAGGACTCCCGCGCAAGCAGCGCGCGTTCGTCGCTGACGTTCCGGG 3019  
Qy 158 ValAspGluAla-----GluLeuValGlyPheSerAspSerLysLysArgLeu 173  
Db 3020 ATGACGACGCTGCTGTCAGCGCGCGCTGTTGAGGAGATATTCGATGCAAAAGCTC 3079  
Qy 174 LeuGluMetIleAspThrAsnAlaAsnAspGlyPro-----AlaLysValIleCysValVal 192  
Db 3080 GTCCGGTGGCTG-----GCCGACGCGGAGCGGAGCTCAAGTGGCTTCCATTGTT 3130  
Qy 193 GlyMetGlyLeuGlyLysThrAlaLeuSerArgLysIlePheGluSerGlu-----Glu 211  
Db 3131 GGATCCGAGGTGTCGCAAGACGACGCTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAG 3190  
Qy 212 AspIleArgLysAsnPheProCysAsnAlaTrpIleThrValSerGlnSerPheHisArg 231  
Db 3191 CGGTTGATGCGCGTTCGACTGCGCGGCTTTCGTCGCGAGCGCGCGAGCGCTGACATG 3250  
Qy 232 IleGluLeuLysAspMetIleArgGlnLeuLeuGlyProSerSerLeuAspGluLeu 251  
Db 3251 ACGAAGATCTCTCAACGACATGCTGTGCACAGCTG-----CGGCCA 3289

Qy 252 LeuGlnGluLeuGlnGlyLysValValValGlnValHisLysLeuSerGluTyrLeuIle 271  
Db 3290 CAACATCAGCATCAGTCTTCGGAGTGTGGAGGTTCATGACCTCTTGAACATATCCGG 3349  
Qy 272 GluGluLeuLysGluLysArgTyrPheValValLeuLeuAspAspLeuTrpIleLeuHisAsp 291  
Db 3350 ACGCATTTGCAGATTAAGAGTACTTCATCATATTAAGATTTATGGCTTCATCAATG 3409  
Qy 292 TrpAsnTrpIleAsnGluIleAlaPheProLysAsnAsnLysLysGlySerArgIleVal 311  
Db 3410 TGGGATATTGTTAGCCGT---GGTTGCTCGATAATAAT---AGTTGCAAGTAGAATACTA 3463  
Qy 312 IleThrThrArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeuValTyrHis 331  
Db 3464 ATAACAACAGAAATGAACCTGTAGCTTGGCATGCTGTGGATATAACTCAGAGCACATT 3523  
Qy 332 LeuAspPheLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArgLysThrAsnLysAsn 351  
Db 3524 ATTAAGATTGATCCCACTGGGTGATGATGTCCTCAAGTCAATTGTTTTCAGTGGAGTGT 3583  
Qy 352 HisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIleValAsnLys 371  
Db 3584 GGCCAAGGAATGAATTCCTGGACATCTTCTCAAGTTCCTCATGACATGATAAATAA 3643  
Qy 372 CysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrLysGlnVal 391  
Db 3644 TGTGGTGGCTTCCCACTAGCAATA---ACTATACAGCCAGACATTTTAAAGCCAGCTG 3700  
Qy 392 SerGluTrpGluLysPheTyrGluHisLeu-----ProSerGluLeuGlu 406  
Db 3701 TTAGATGAATGCACCAATGAATCATACATAAAATCATGTACTTCCATTTGAAG 3760  
Qy 407 IleAsnProSerLeuGluAlaLeuArgArgMetValThrLeuGlyTyrAsnHisLeuPro 426  
Db 3761 AAAAACTCTACTTTCAGGGGATGAGGAGTACTCAACCTTATTACATAATATCTCT 3820  
Qy 427 SerHisLeuLysProCysPheLeuTyrLeuSerIlePheProGluAspPheGluIleLys 446  
Db 3821 CATTTGTTGAAGCATGCTGTTATACCTTAGCATCTCAAGAGGACTACATAATAGG 3880  
Qy 447 ArgAsnArgLeuValGlyArgTrpIleAlaGlyLysIleLysThrCysArgIleHisAspIleArg 506  
Db 3881 AAGGCCAACTTGGTGAGCAATGATGGCTGCAAGTTCATCAATCCATAGAAAAATAA 3940  
Qy 467 ThrThrLysAspValGlyLysTyrPheAsnGluLeuIleAsnArgSerMetIleGln 486  
Db 3941 GTCATGGAAGAAGTTGAGGGAATATTTGATGAATCTTGTGGTAGGGCCCTGGTCCAA 4000  
Qy 487 ArgSerArgValGlyIleAlaGlyLysIleLysThrCysArgIleHisAspIleArg 506  
Db 4001 CCAGTAGATGTTAACTGCAAAATGAGGTATTGTGATGTAGTCAGCACCATGTTATTA 4060  
Qy 507 AspIleThrValSerIleSerArgGlnGluAsnPhe---ValLeuLeuProMetGlyAsp 525  
Db 4061 AATTCATCAGGTGAAGTCAATAGAGAGAAATTCAGCATTAATGATGATCTCTCAG 4120  
Qy 526 GlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHisGlySerMetSerCys 545  
Db 4121 ACGACAGTAAGACATGTCGCAAGGTTCCGCGACTCTCGCTTCACTTCAGCAATGCACAT 4180  
Qy 546 LysThr-----GlyLeuAspTrpSerIleLeuArgSerLeuAlaIlePheGly 561  
Db 4181 GATACAAACACCACTAGCAGGTTTGAGACTCTCAAGTTCGATCGATGGCATTTTTCGA 4240  
Qy 562 AspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeu-----ArgMet 578  
Db 4241 -----CAAGTCAAGTGTATGCTTCCATTCAGATTATAGGCTT 4279  
Qy 579 LeuArgValLeu-----AspLeuGluAspValThrPheLeuIleThr 592  
Db 4280 TTTCCGAGTTCTGATCTTTTGTGTTTGGGCTGATCAGAGAAACAAAGCTAT----- 4330

QY 593 GlnLysAspPheAspArgIleAlaLeuLeuCysHisLeuLysTyrLeuSerIleGlyTyr 612  
DB 4331 -----GACCTCACAAGCATTTTGAACCTGTGTACAACTGAGATATCTGAAGATAACAGGT 4384  
QY 613 SerSerSerIleTyrSerLeuProArgSerIleGlyLeuGlnGlyLeuGlnThrLeu 632  
DB 4385 AATATCACAGTT---AACTTCCAGAGAGATCCAGGACTACACACTTGCAGACATG 4441  
QY 633 AsnMetProSerThrTyrIleAlaLeuProSerGluSerIleSerLysLeuGlnCysLeu 652  
DB 4442 GAAGCAGATGCAAGAGCAACTGCTGTCTTA---TTGGATATTCTTCATACACAGTGTG 4498  
QY 653 HisThrLeuArgCysIleGlyGlnPheHisTyrAspAsnPheSerLeuAsnHisProMet 672  
DB 4499 TTGCACCTTCGCTTGTGA----- 4516  
QY 673 LysCysIleThrAsnThrIle-----CysLeuProLysValPheThrProLeuValSer 690  
DB 4517 -----CTACTTGATCTGCTCCCTCACTGTACAGGTACATCTTACC----- 4558  
QY 691 ArgAspAspArgAlaLysGlnIleAlaLeuLeuHisMetAlaThrLysSerCysTrpSer 710  
DB 4558 ----- 4559  
QY 711 GluSerIleCysValLysValProLysGlyIleGlyLysLeuArgAspLeuGlnValLeu 730  
DB 4559 -----AGCATCCCAATGAGTGAAGCTCAACAATCTCCGCAATTTA 4603  
QY 731 GluTyrValAspIleArgArgThrSerSerArgAlaIleLysGlnLeuGlnLeuSer 750  
DB 4604 AACATT-----CGATCATGCATAAATTTCCAG----- 4630  
QY 751 LysLeuArgLysLeuGlyValThrThrAsnGlySerThrLysGluLysCysLysIleLeu 770  
DB 4630 ----- 4631  
QY 771 TyrAlaAlaIleGluLysLeuSerSerLeuGlnSerLeuHisValAspAlaAlaGlyIle 790  
DB 4630 ----- 4631  
QY 791 SerAspGlyGlyThrLeuGluCysLeuAspSerIleSerSerProProLeuLeuArg 810  
DB 4631 GATGACTTGCACCTCTCAAGGACTGGGATCTCTCACTGCTTTTCGCTGCTTGTGA 4690  
QY 811 ThrLeuValLeuAspGlyIleLeuGluMetProAsnTrpIleGluGlnLeuThrHis 830  
DB 4691 ACAGCGCTTCGCAAGAATCGTC----- 4714  
QY 831 LeuLysLysIleTyrLeuLeuArgSerLysLeuLysGluGlyLysThrMetLeuLeu 850  
DB 4715 -----CTCGAATGAGGG-----TTC 4732  
QY 851 GlyAlaLeuProAsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLys 870  
DB 4733 GGGTCTCTCAAGTACTTCAATGTTGTC-----TGTACAGCACCATGC 4774  
QY 871 LeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyrGluLeuAsp 890  
DB 4775 ATCATTTTGTGAAGAGCAATGCCGAGTGTGCAAGTTA----- 4816  
QY 891 GlnLeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGluIle 910  
DB 4817 -----AATCTAAGGTTCAATGCCAACGAGTTCAAG----- 4846  
QY 911 GlyLysCysArgLeuSerGlyIleThrGlyIleIleHisLeuProLysLeuLysGlu 930  
DB 4847 -----CAGTATGACTTCAAGGAGACAGGTTGGACACTTGTGCGCCCTTCAGAG 4897  
QY 931 IleProIleArgTyrGly-----SerLysValAlaGlyLeuGly 943  
DB 4898 ATCTCTCAAGAAATTCGGGGCACTGATGATGATGAATCAACAAACTGAAGTGGAGTCT 4957  
QY 944 GlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeuMetTyrSerAsp 963

DB 4958 GCCTTGAGGACTGCATTCGAATTCGAACATCCCAAGCCGAGCACTCTTATGGTT-----GAT 5011  
QY 964 ArgArgTyrHisAspLeuGlyAlaGluAlaGluGlySerSerIleGluValGlnThrAla 983  
DB 5012 ATACAATGGGTGGATTGGATCTTTGGTGTCTGAAGGAGAGACTTGGATGAAGATTGGCA 5071  
RESULT 4  
US-09-993-170-57  
; Sequence 57, Application US/09993170  
; Patent No. 6743969  
; GENERAL INFORMATION:  
; APPLICANT: Valant, Barbara  
; APPLICANT: Bryan, Gregory  
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene  
; TITLE OF INVENTION: Specificity and Method for Engineering Altered  
; TITLE OF INVENTION: Specificity  
; FILE REFERENCE: BB1385 US NA  
; CURRENT APPLICATION NUMBER: US/09/993,170  
; CURRENT FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 60/248,335  
; PRIOR FILING DATE: 2000-11-14  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 57  
; LENGTH: 5222  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-09-993-170-57  
Alignment Scores:  
Pred. No.: 6,48e-61 Length: 5222  
Score: 637.50 Matches: 256  
Percent Similarity: 40.0% Conservative: 168  
Best Local Similarity: 24.2% Mismatches: 381  
Query Match: 12.1% Indels: 255  
DB: 3 Gaps: 35

US-10-656-394A-8 (1-1032) x US-09-993-170-57 (1-5222)

QY 1 MetalAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20  
DB 2426 ATGGCGCGCGGGTCAATTCATCGAGGTGTCTCATCGCGGTCCCTGACGAGCAAGCTC 2485  
QY 21 AlaSer-----AlaAlaAlaAspGluThrSerLeuLeu 31  
DB 2486 GACTCGCTGTGTCGACGCCCGCGCGCTCGCAACCGTCTGCTGCTGCGG 2545  
QY 32 LeuGlyValGluLysAspIleTrpTyrIleLysAspGluLeuLysThrMet-----Gln 49  
DB 2546 AAGGGGAGAGAGAGAGAGATCTCTCTCAGAGGCGATCTCCGACACCTGTAGATGAC 2605  
QY 50 AlaPheLeuArgAla-----AlaGluLeuMetLysLysAspGluLeuLeuLys 66  
DB 2606 TACTACCTCTCTGTCGAGCCCGCTCAGACACCGCCGCCACCGCAGCTCGACGGCGGCG 2665  
QY 67 ValTTPAlaGluGlnIleArgAspLeuSerTyrAspIleGluAspSerLeuAspGluPhe 86  
DB 2666 TGTGGGCTTAAGGAGTTCGGAGCTCTCTCTACGACGTGACGACGACTCTCTCGACGAGCTA 2725  
QY 87 LysValHisIle----- 90  
DB 2726 ACGACCCAGCTCTCTCCACCGCGCGCGGCGATGGAGTAGTACACTGCTGTGTCGAAG 2785  
QY 91 -----GluSerGlnThrLeuPheArgGlnLeuValLysLeuArgGluArgHisArgIle 108  
DB 2786 AAGATGATCAGCAGCATGATCGCGCGCTTCGAGGGGAGCTTAACCGCGCGCGGTGATC 2845  
QY 109 AlaIleArgIleHisAsnLeuLysSerArgValGluValSerSerArgAsnThrArg 128  
DB 2846 GCCGACGAGGTTCACCTCTTCAGGGCGCGCGTGAAGGAGGCCATTCGCCGCCACGAGAC 2905  
QY 129 TyrSerLeuValLysProIleSerSerGlyThrGluIleAspMetAspSerTyrAlaGlu 148

Db 2906 TACCATTCTGGCAGGCGCACCTCGAGCTCGAGGCGGAGAGAGACGAC-----GAC 2959  
Qy 149 AspIleArgAsnGlnSerAlaAlaArgAsn----- 157  
Db 2960 GACGATCGCGAGGACTCGCGCGCAACGAGCGCGCGTTCCTGCTCGCTGAGCTTCGGG 3019  
Qy 158 ValAspGluAla-----GluLeuValGlyPheSerAspSerLysLysArgLeu 173  
Db 3020 ATGGACGAGCTGCTGTCGCGCGCGCTGCTGCTGAGGATATTCGATGCAAGAGCTC 3079  
Qy 174 LeuGluMetIleAspThrAsnAlaAsnAspGlyPro---AlaLysValIleCysValVal 192  
Db 3080 GTCCGGTGGCTG-----GCCGAGCGCGGCGAAGCTCAAGGTGGCTTCATTGTT 3130  
Qy 193 GlyMetGlyLeuGlyLeuThrAlaLeuSerArgLysIlePheGluSerGlu---Glu 211  
Db 3131 GGATCCGAGGTGTTGGCAGAGCAGCGCTGGCCACAGATTCATGCTGTCGATGCGCGG 3190  
Qy 212 AspIleArgLysAsnPheProCysAsnAlaTrpIleThrValSerGlnSerPheHisArg 231  
Db 3191 CGGTTGCATCGCGCTTCGACTGCGCGCTTCGTCGCGAGCGCGCGAGCGCTGACATG 3250  
Qy 232 IleGluLeuLeuLysAspMetIleArgGlnLeuLeuGlyProSerSerLeuAspGlnLeu 251  
Db 3251 ACGAAGATCCTCACCGACATGCTGCACAGCTG-----CGGCCA 3289  
Qy 252 LeuGlnGluLeuGlnGlyLysValValGlnValHisLeuSerGluTrpLeuLeu 271  
Db 3290 CAACATCAGCATCAGTCTCGAGTGTGGAGGTTCATCGCTCTGAACTATCCGG 3349  
Qy 272 GluGluLeuLysGluLysArgTrpPheValValLeuAspAspLeuTrpIleLeuHisAsp 291  
Db 3350 ACCATTTTCAGAGATAAAGGTACTTCATCATATTCAGATTTATGGCTTCATCAATG 3409  
Qy 292 TrpAsnTrpIleAsnGluLeuAlaPheProLysAsnLeuLysGlySerArgIleVal 311  
Db 3410 TGGATATTTAGCCGT---GGTTTGCCTGATATAAT---AGTTGCAGTAGATACTA 3463  
Qy 312 IleThrThrArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeuValTrpHis 331  
Db 3464 ATAAACACAGAAATGAACCTGTAGCTTTGGCATGTGCTGGATATAACTCAGACGACAT 3523  
Qy 332 LeuAspPheLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArgLysThrAsnLysAsn 351  
Db 3524 ATTAAGATTGATCCAGTGGTGATGATGCTCAAGTCAATTTGTTTCAGTGGAGTTGT 3583  
Qy 352 HisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIleValAsnLys 371  
Db 3584 GGCCAGGAAATGAATTTCTCGACATCTTACTGAGTTTCTCATGACATGATAAAAAA 3643  
Qy 372 CysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrLysGlnVal 391  
Db 3644 TGTGGTGGCTTCCACTAGCAATA---ACTATAACAGCCAGACATTTAAAGCCAGCTG 3700  
Qy 392 SerGluTrpGluLysPheTrpGluHisLeu-----ProSerGluLeuGlu 406  
Db 3701 TTAGATGGAAATGCAATGGAATCACAATAAATCAATCAATCAATTTTGAAG 3760  
Qy 407 IleAsnProSerLeuGluAlaLeuArgArgMetValThrLeuGlyTrpAsnHisLeuPro 426  
Db 3761 AAAATCCTACTTTGACGGGATGAGGAGTACTCAACCTTATTTACATATATCTTCT 3820  
Qy 427 SerHisLeuLysProCysPheLeuTrpLeuSerIlePheProGluAspPheGluLeuLys 446  
Db 3821 CATTTGTTGAAAGCATGCTGTATATCCTTAGCATCTACAAAGAGGACTACATAATTAGG 3880  
Qy 447 ArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheValArgProLysValGlyMet 466  
Db 3881 AAGGCCAATCTGGTACGCAATGATGGCTGAGGTTTTCATCAATTCATAGAAATAAA 3940  
Qy 467 ThrThrLysAspValGlyGluSerTrpPheAsnGluLeuLeuAsnArgSerMetIleGln 486  
Db 4691 ACAGCGCTCGCGCAAGAAATCGTC----- 4714

Db 3941 GTCATGGAGAAAGTTGCGAGGAACACTATTTGATGAACACTTCTGCTAGGGCCCTGGTCCAA 4000  
Qy 487 ArgSerArgValGlyIleAlaGlyLysIleLeuThrCysArgIleHisAspIleLeuArg 506  
Db 4001 CCAGTAGATGTTAACTGCAAAATAGAGTATTTGTCATGCTAGTCAGCACCATGTTATTA 4060  
Qy 507 AspIleThrValSerIleSerArgGlnGluAsnPhe---ValLeuLeuProMetGlyAsp 525  
Db 4061 AATTTTCATCAGGTGTAAGTCAATAGAGAGAAATTTGAGATTCATTCATTCATTCAG 4120  
Qy 526 GlySerAspLeuValGlnGlnGluAsnThrArgHisIleAlaPheHisGlySerMetSerCys 545  
Db 4121 ACGACAGTAAGACATGCTGACAGGTTGCGCGACTCTCGCTTCACCTTCAGCAATGCACAT 4180  
Qy 546 LysThr-----GlyLeuAspTrpSerIleLeuArgSerLeuAlaIlePheGly 561  
Db 4181 GATACACACCATCAGCAGGTTTGAGACTCTCAAGTTCGATCGATGCGATTTTCGGA 4240  
Qy 562 AspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeu-----ArgMet 578  
Db 4241 -----CAAGTCAAGTGTATGCTTCCATTTCAGATTATAGGCTT 4279  
Qy 579 LeuArgValLeu-----AspLeuGluAspValThrPheLeuLeuThr 592  
Db 4280 TTTTCAGTTCTGATTCCTTTGTTGCTGATCAAGAGAAACAACAGCTAT----- 4330  
Qy 593 GlnLysAspPheAspArgIleAlaLeuLeuCysHisLeuLysTrpLeuSerIleGlyTrp 612  
Db 4331 -----GACCTCACACAGCATTTTGAACCTGTACAACTGAGATATCTGAAGATAACAGT 4384  
Qy 613 SerSerSerIleTrpSerLeuProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeu 632  
Db 4385 AATATCACAGTT---AAACTTCCAGAGAGATCCAGGACTACAACACTTCGACAGACTG 4441  
Qy 633 AsnMetProSerThrTrpIleAlaLeuProSerGluIleSerLysLeuGlnCysLeu 652  
Db 4442 GAAGCAGATGCAAGAGCACTGCTGCTTA---TTGGATATTGTTTCATACACAGTGTG 4498  
Qy 653 HisThrLeuArgCysIleGlyGlnPheHisTrpAspAsnPheSerLeuAsnHisProMet 672  
Db 4499 TTGCACCTTCCTCTGTA----- 4516  
Qy 673 LysCysIleThrAsnThrIle-----CysLeuProLysValPheThrProLeuValSer 690  
Db 4517 -----CTACTGTGATCTGCTCCCTCACTGTCACAGGTACATCTTCACC----- 4558  
Qy 691 ArgAspAspArgAlaLysGlnIleAlaGluLeuHisMetAlaThrLysSerCysTrpSer 710  
Db 4558 ----- 4558  
Qy 711 GluSerIleGlyValLysValProLysValProLysGlyIleGlyLysLeuArgAspLeuGlnValLeu 730  
Db 4559 -----ACCATCCCAATGAGCTGGAAGACTCAACAACTTCGCAATTTA 4603  
Qy 731 GluTrpValAspIleArgArgThrSerArgAlaIleLysGluLeuGlyGlnLeuSer 750  
Db 4604 AACATT-----GCAGTCATGCAAAATTTCCAG----- 4630  
Qy 751 LysLeuArgLysLeuGlyValThrThrAsnGlySerThrLysGluLysCysLysIleLeu 770  
Db 4630 ----- 4630  
Qy 771 TyrAlaAlaIleGluLysLeuSerSerLeuGlnSerLeuHisValAspAlaGlyIle 790  
Db 4630 ----- 4630  
Qy 791 SerAspGlyGlyThrLeuGluCysLeuAspSerIleSerSerProProLeuLeuArg 810  
Db 4631 GATGACCTTGACACTCTCAAGAGCTGGGATCTCTCAGCTCTTTCGCTGCTGTTTGA 4690  
Qy 811 ThrLeuValLeuAspGlyIleLeuGluMetProAsnTrpIleGluGlnLeuThrHis 830  
Db 4691 ACAGCGCTCGCGCAAGAAATCGTC----- 4714

QY 831 LeuLysLysIleTyrLeuLeuArgSerLysLeuLysGluGlyLysThrMetLeuLeu 850  
Db 4715 -----GCTCGGAATGAGGG-----TTC 4732  
QY 851 GlyAlaLeuProAsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyLys 870  
Db 4733 GGGTCTCTCAAGTACTTTCATCTTGTTC-----TGTACACACCATGC 4774  
QY 871 LeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeuTyrPheTyrGluLeuAsp 890  
Db 4775 ATGACTTTTGTGAGAGGAGCAATGCCAGTGTGCAAGGTTA----- 4816  
QY 891 GlnLeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGluIle 910  
Db 4817 -----AATCTAAGGTTCAATGCCAACGAGTTCAG----- 4846  
QY 911 GlyGluCysArgLeuGluSerGlyIleThrGlyIleIleHisLeuProLysLeuLysGlu 930  
Db 4847 -----CAGTATGACTTAAGGAGACAGGGTGTGAACACTTGTTCGCCCTTGCAGAG 4897  
QY 931 IleProIleArgTyrGly-----SerLysValAlaGlyLeuGly 943  
Db 4898 ATCTCTGCAAGAATTTGGGGCAGCTGATGATGATGAATCAACAACAACTCAAGTGGAGTCT 4957  
QY 944 GlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeuMetTyrSerAsp 963  
Db 4958 GCCTTGAGACTGCAATTCGACAGATCCGACGCGGAGCACTCTTATGGTT-----GAT 5011  
QY 964 ArgArgTyrHisAspLeuGlyAlaGluGlySerSerIleGluValGlnThrAla 983  
Db 5012 ATACATGGTGGTATGATCTTTGGTCTGACGAGGAGACTTGGATGAAGATTGGCA 5071

## RESULT 5

US-09-993-170-60  
; Sequence 60, Application US/09993170  
; Patent No. 6743969  
; GENERAL INFORMATION:  
; APPLICANT: Bryant, Gregory  
; TITLE OF INVENTION: Modification of a Plant Disease Resistance Gene  
; TITLE OF INVENTION: Specificity and Method for Engineering Altered  
; TITLE OF INVENTION: Specificity  
; FILE REFERENCE: BH1385 US NA  
; CURRENT APPLICATION NUMBER: US/09/993,170  
; PRIOR FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 60/248,335  
; PRIOR FILING DATE: 2000-11-14  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 60  
; LENGTH: 5696  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Chimeric Gene  
US-09-993-170-60

Alignment Scores:  
Pred. No.: 7.58e-61 Length: 5696  
Score: 637.50 Matches: 256  
Percent Similarity: 40.0% Conservative: 168  
Best Local Similarity: 24.2% Mismatches: 381  
Query Match: 12.1% Indels: 255  
DB: 3 Gaps: 35

US-10-656-394A-8 (1-1032) x US-09-993-170-60 (1-5696)

QY 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20  
Db 2426 ATGGCGCGCGGCTCATTCATCGCAGGAGTGTGTCATCATCGGTCTCCCTGACGACGAAGCTC 2485  
QY 21 AlaSer-----AlaAlaLeuAspGluThrSerLeuLeu 31

Db 2486 GACTCGCTGCTGTCAGCCGCGAGCCGCCGCCCTCGCGAACCGTCTGCTGCTGCGG 2545  
QY 32 LeuGlyValGluLysAspIleTyrTyrIleLysAspGluLeuLysThrMet-----Gln 49  
Db 2546 AAGGGGAGAGAGAAAGACTCTCTCTCTCAGAGGCGATCTCCGACACACCTGTAGATGAC 2605  
QY 50 AlaPheLeuArgAla-----AlaGluLeuMetLysLysLysAspGluLeuLys 66  
Db 2606 TACTACCTCTCTGTCGAGCCGCGCTCAGACACCGCCGCCACCCGACACTCGACGGCGGG 2665  
QY 67 ValTyrAlaGluGlnIleArgAspLeuSerTyrAspIleGluAspSerLeuAspGluPhe 86  
Db 2666 TCGTGGCTTAAGAGGTTTCGAGCTCTCTCTACGAGCTCGACGACTCTCTCGACGAGCTA 2725  
QY 87 LysValHisIle----- 90  
Db 2726 ACGACCCAGCTCTCCACACCGCGCGCGGCGAGTGGCAGTAGCTGCTGTTGCCAAG 2785  
QY 91 -----GluSerGlnThrLeuPheArgGlnLeuValLysLeuArgGluArgHisArgIle 108  
Db 2786 AAGATGATCAGCAGCATGATCGCGCGCTTCGAGGGAGCTTAACCGCGCGGTGGATC 2845  
QY 109 AlaIleArgIleHisAsnLeuLysSerArgValGluValSerSerArgAsnThrArg 128  
Db 2846 GCCGACGAGGTCACTCTGTTTCAGGGCGCGCTGAAGAGGCCATTCCGCCGCCACGAGAGC 2905  
QY 129 TyrSerLeuValLysProIleSerSerGlyThrGluIleAspMetAspSerTyrAlaGlu 148  
Db 2906 TACCATCTTGGCAGGCGCACCTCGAGTTCGAGGCCGAGAGAGAACGACGAC-----GAC 2959  
QY 149 AspIleArgAsnGlnSerAlaArgAsn----- 157  
Db 2960 GACGATCGCAGGACTCCGCGCGCAACGACGCGCGGTTCCTGCTGCTGAGTTCGGG 3019  
QY 158 ValAspGluAla-----GluLeuValGlyPheSerAspSerLysLysArgLeu 173  
Db 3020 ATGGACGAGCTGTGTGTCAGCGCCAGCTGTTGGTAGGATATTTCGATGCAAAAGCTC 3079  
QY 174 LeuGluMetIleAspThrAsnAlaAsnAspGlyPro-----AlaLysValIleCysValVal 192  
Db 3080 GTCCGGTGGCTG-----GCCGAGCGGCGAGCCGAAAGCTCAAGGTGCTTCATTGTT 3130  
QY 193 GlyMetGlyGlyLeuGlyLysThrAlaLeuSerArgLysIlePheGluSerGlu-----Glu 211  
Db 3131 GGATCCGAGGTTGTGGACAGCACCTCGCCACAGAAATCTATGCTGTCATGCCCGG 3190  
QY 212 AspIleArgLysAsnPheProCysAsnAlaTyrPheThrValSerGlnSerPheHisArg 231  
Db 3191 CGGTTGGATGCGCGCTTCGACTGCGGGCTTTCGTGCGAGCGCCCGGAGGCTGACATG 3250  
QY 232 IleGluLeuLysAspMetIleArgGlnLeuGlyProSerSerLeuAspGlnLeu 251  
Db 3251 ACGAAGATCTTCACGACATCTCTCACAGCTG-----CGGCCA 3289  
QY 252 LeuGlnGluLeuGlnGlyLysValValValGlnValHisHisLeuSerGluTyrLeuIle 271  
Db 3290 CAACATCAGCATCAGTCTTCGATGTTTGGAGGTTGATCGACTCTCTGAAATATCCGG 3349  
QY 272 GluGluLeuLysGluLysArgTyrPheValValLeuAspAspLeuTyrPheLeuHisAsp 291  
Db 3350 ACGCATTTGCAAGATAAAGGTACTTCATCAATTTGAAGATTTATGGGCTTCATCAATG 3409  
QY 292 TyrAsnTyrPheAsnGluIleAlaPheProLysAsnAsnLysLysGlySerArgIleVal 311  
Db 3410 TGGGATATTGTTAGCCGT---GGTTTCTCTGATAATAAT---AGTTGCAGTAGAATACTA 3463  
QY 312 IleThrThrArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeuValTyrHis 331  
Db 3464 ATAACAACAAGAAATGAACCTTGGATCTGTCATGATATACATCAGACGACAT 3523  
QY 332 LeuAspPheLeuGlnMetAsnAlaIleThrLeuLeuLeuArgLysThrSerLeuAsn 351

Db 3524 ATTAAGATTGATCCACTGGGTGATGATGCTCAAGTCAATTTGTTTTTCACTGAGTTGTT 3583  
Qy 352 HisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIleValAsnLys 371  
Db 3584 GGCACAGGAATGAATTTCTCTGACATCTTACTGAAGTTTCTCATGACATGATAAAAAA 3643  
Qy 372 CysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrLysGlnVal 391  
Db 3644 TGTGTGGCTTGGCACTAGCATA---ACTATACAGCCAGACATTTTAAAGCCAGCTG 3700  
Qy 392 SerGluTrpGluLysPheTyrGluHisLeu-----ProSerGluLeuGlu 406  
Db 3701 TTAGATGGAATGAGCAATGGAATCACAATACAAAATCAATTTGCACTACTTCCATTTGAAG 3760  
Qy 407 IleAsnProSerLeuAlaLeuArgArgMetValThrLeuGlyTyrAsnHisLeuPro 426  
Db 3761 AAAAACTTACTTTGCGGGGATGAGGCACTCAACCTTATTACATATATCTTCT 3820  
Qy 427 SerHisLeuLysProCysPheLeuTyrLeuSerIlePheProGluAspPheGluIleLys 446  
Db 3821 CATTTGTTGAAAGCATGCTGTATACCTTAGCATCTACAAAGAGGACTACATAATTAGG 3880  
Qy 447 ArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheValArgProLysValGlyMet 466  
Db 3881 AAGGCCAATTGTTGGGCAATGGATGGCTGAGGTTTCAATTCATCCATAGAAATAAA 3940  
Qy 467 ThrThrLysAspValGlyGluSerTyrPheAsnGluLeuIleAsnArgSerMetIleGln 486  
Db 3941 GTCATGGAAGAAGTTGCAGGAACTATTATTGATGAATTTGTTGGTGGGCGCTGGTCCAA 4000  
Qy 487 ArgSerArgValGlyIleAlaGlyLysIleLysThrCysArgIleHisAspIleLeuArg 506  
Db 4001 CCACTAGATGTTAACTGCMAAATGAGTATTGTCATGTAGTGCACCACTAGGTATTA 4060  
Qy 507 AspIleThrValSerIleSerArgGlnGluAsnPhe---ValLeuLeuProMetGlyAsp 525  
Db 4061 AATTTTCATCAGGTGAAGTCAATAGAGGAAATTTAGCATTTACATTTGATCTCAG 4120  
Qy 526 GlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHisGlySerMetSerCys 545  
Db 4121 ACACAGTAAAGACATGTCAGAGGTTCCGCGATCTCGCTTCACTTCAGCAATGCACAT 4180  
Qy 546 LysThr-----GlyLeuAspTrpSerIleIleArgSerLeuAlaIlePheGly 561  
Db 4181 GATACACACCACCTAGCAGGTTTGAGACTCTCACAGTTCGATCGATGTCATTTTGGCA 4240  
Qy 562 AspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeu-----ArgMet 578  
Db 4241 -----CAAGTCAAGTGTATGCTTCCATTCGAGATTATAGGCTT 4279  
Qy 579 LeuArgValLeu-----AspLeuGluAspValThrPheLeuIleThr 592  
Db 4280 TTTTCGAGTTCTGATTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4330  
Qy 593 GlnLysAspPheAspArgIleAlaLeuLeuCysHisLeuLysTyrLeuSerIleGlyTyr 612  
Db 4331 -----GACCTCACAGCATTTTGAAGTGTATCAACTGAGATATCTGAAGATAACAGT 4384  
Qy 613 SerSerIleTyrSerLeuProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeu 632  
Db 4385 AATATCACAGTT---AAATCCAGAGAGATCCAGGACTACACACTTGCAGACACTG 4441  
Qy 633 AsnMetProSerThrTyrIleAlaLeuProSerGluIleSerLysLeuGlnCysLeu 652  
Db 4442 GAAGCAGATGCAAGAGCAACTGCTGTCTTA---TTGATATTTTTCATACAGAGTTTG 4498  
Qy 653 HisThrLeuArgCysIleGlyGlnPheHisTyrAspAsnPheSerLeuAsnHisProMet 672  
Db 4499 TTGCACCTTCGCTTGTGA----- 4516  
Qy 673 LysCysIleThrAsnThrIle-----CysLeuProLysValPheThrProLeuValSer 690  
Db 4517 -----CTACTTGATCTGCTCCCTCCTGTCACAGGTACATCTTCACC----- 4558

Qy 691 ArgAspArgAlaLysGlnIleAlaGluLeuHisMetAlaThrLysSerCysTrpSer 710  
Db 4558 ----- 4558  
Qy 711 GluSerIleGlyValLysValProLysGlyIleGlyLysLeuArgAspLeuGlnValLeu 730  
Db 4559 -----AGCATCCCAATGAGTGGGAAGCTCAACATCTCCGCATTTTA 4603  
Qy 731 GluTyrValAspIleArgArgThrSerSerArgAlaIleLysGluLeuGlyGlnLeuSer 750  
Db 4604 AACATT-----GCAGTCATGCAAAATTTCCAG----- 4630  
Qy 751 LysLeuArgLysLeuGlyValThrThrAsnGlySerThrLysGluLysCysLysIleLeu 770  
Db 4630 ----- 4630  
Qy 771 TyrAlaAlaIleGluLysLeuSerSerLeuGlnSerLeuHisValAspAlaGlyIle 790  
Db 4630 ----- 4630  
Qy 791 SerAspGlyGlyThrLeuGluCysLeuAspSerIleSerSerProProLeuLeuArg 810  
Db 4631 GATGACCTTGACACTCTCAAGGACTGGGATCTCTCACTGCTCTTCGCTGCTGTTCGA 4690  
Qy 811 ThrLeuValLeuAspGlyIleLeuGluGluMetProAsnTrpIleGluGlnLeuThrHis 830  
Db 4691 ACAGCGCCTGGCCAAAGAAATCGTC----- 4714  
Qy 831 LeuLysLysIleTyrLeuLeuArgSerLysLeuLysGluGlyLysThrMetLeuIleLeu 850  
Db 4715 -----GCTGCCAATGAGGG-----TTC 4732  
Qy 851 GlyAlaLeuProAsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLys 870  
Db 4733 GGGTCTCTCAAGTACTTCTCATGTTGTC-----TGTCAGCACCATGTC 4774  
Qy 871 LeuValPheLysThrGlyValAlaPheProAsnLeuArgThrLeuTrpIleTyrGluLeuAsp 890  
Db 4775 ATGACTTTTGGGAAGAGCAATCCGAGTGTGCAAGGTTA----- 4816  
Qy 891 GlnLeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGluIle 910  
Db 4817 -----AATCTAAGTTCAATGCCAAGCTTCAAG----- 4846  
Qy 911 GlyGluCysArgLeuGluSerGlyIleThrGlyIleIleHisLeuProLysLeuLysGlu 930  
Db 4847 -----CAGTATGACTCTAAGGACACAGGTTGGAACACTTGTGCTCCCTTGCAGAG 4897  
Qy 931 IleProIleArgTyrGly-----SerLysValAlaGlyLeuGly 943  
Db 4898 ATCTCTGCAAGAAATTTGGGGCCTGATGATGATGAATCAACAACTGAAGTGGAGTCT 4957  
Qy 944 GlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeuMetTyrSerAsp 963  
Db 4958 GCCTTGAGGACTGCAATTCGCAAGCATCCGACCCGACGACACTCTTATGTT-----GAT 5011  
Qy 964 ArgArgTyrHisAspLeuGlyAlaGluAlaGluGlySerSerIleGluValGlnThrAla 983  
Db 5012 ATACAATGGGTGGATTGATCTTTTGGTGTGTAAGGAGAGAGACTTGGATGAAGATTTGGCA 5071

## RESULT 6

US-09-360-186-2  
; Sequence 2, Application US/09360186  
; Patent No. 6262343  
; GENERAL INFORMATION:  
; APPLICANT: Staskawicz, et al.  
; TITLE OF INVENTION: B2 Resistance Gene  
; FILE REFERENCE: 50687  
; CURRENT APPLICATION NUMBER: US/09360,186  
; CURRENT FILING DATE: 1998-07-23  
; EARLIER APPLICATION NUMBER: 60/093,957  
; EARLIER FILING DATE: 1998-07-23







Db 327 CAACTGAGACTAACAGGAACCTGTACTGGGAGAAAAATAAAGCCAGAAAAAAGGCGGT 386  
Qy 125 AtgAsnThrArgTyrSerLeu----- 131  
Db 387 CGAAGGTTTCGTCAAAGCTGCAACAGTACGAGGACATCATATCTCGAAGAG 446  
Qy 132 ---VallyProIleSerSerGlyThrGluIleAspMetAspSerTyrAlaGluAspIle 150  
Db 447 TCGACAAAGATCCAGATAAAGGAAACAAAGTATCAAAAGGAATCATTTGTTTCATGATTTT 506  
Qy 151 ArgAsnGlnSerAlaArgAsnValAspGluAlaGlu-----LeuValGlyPheSerAsp 168  
Db 507 ---TCAAGTTCACAAACGATATTTTGAAGGTGAAGCAATATGTTGGAGCTGATGAT 563  
Qy 169 SerLysArgLeuLeuGluMetIleAspThrAsnAlaAsnAspGlyProAlaLysVal 188  
Db 564 CAAAGGAAACAGTTGTTAGAGATCTG---ACTAGAAGCTACTCTGGGGAACCCAAAGTC 620  
Qy 189 IleCysValValGlyMetGlyGlyLeuGlyLysThrAlaLeuSerArgLysIlePheGlu 208  
Db 621 ATCCGATTTGCGGATGGAGGCGATAGTAAACACCTTAGCAAAAGAGTTTAC--- 677  
Qy 209 SerGluGluAspIleArgLysAsnPheProCysAsnAlaTrpIleThrValSerGlnSer 228  
Db 678 AATGATGAATCAATTCATCGCGTTTGTATGTTTCATGCTCGGCTACCATATCTCAACAG 737  
Qy 229 PheHisArgIleGluLeuLeuLysAspMetIleArgGlnLeuLeuGlyProSerSerLeu 248  
Db 738 CACAAACAAAGAAATTTTGTGGGCTTCTGATTCATGCTCGGCTACCATATCTCAACAG 797  
Qy 249 AspGlnLeuGlnGluLeuGlnGlyLysValValGlnValHisLeuSerGlu 268  
Db 798 GTTAAGATGATTGTTGAACGACAG-----CTAGCAGAC 830  
Qy 269 TyrLeuIleGluLeuLysGlyArgTyrPheValValLeuAspLeuTrpIle 288  
Db 831 ATGTTACAGAAAAGTTTAAAGAGAGAGAGTACTTAATGTCTGGGATATCTCGAGT 890  
Qy 289 LeuHisAspTrpAsnTrpIleAsnGluIleAlaPheProLysAsnAsnLysLysGlySer 308  
Db 891 TGTGAAGTGTGGGTCGCTGAGACGA--TGTCTTCCAACTGAAGACAAATGCGAGGAGT 947  
Qy 309 ArgIleValIleThrArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeu 328  
Db 948 CGAATATGTTGACTACCGGTAATGATGAAGTAGCTTGTATGCTGCTGTAGAGAATTTT 1007  
Qy 329 ValTyrHisLeuAspPheLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArgLysThr 348  
Db 1008 TCTTTGCGATGATGCTTCATGATCAAGATGAGAGTTGGAGT---CTTTTCAAAAGTGCA 1064  
Qy 349 AsnLysAsnHisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIle 368  
Db 1065 GCATTTTCAAGTGAAGCATTACCA-----TATGAGTTTCGAGACTGTTGAAAGCAATC 1118  
Qy 369 ValAsnLysCysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThr 388  
Db 1119 CGAGATGAATGTACCGGTATCACTACTATGTCGTGCTGAGGCTTCTCAATCT 1178  
Qy 389 LysGln---ValSerGluTrpGluLysPheTyrGluHisLeuProSerGluLeuGluIle 407  
Db 1179 AAAGGACATAGAGATTGGAAACTGTTGCTAAAGATGTCAAGTCAATCTCGTCACAAAT 1238  
Qy 408 AsnProSerLeuGluAlaLeuArgMetValThrLeuGlyTyrAsnHisLeuProSer 427  
Db 1239 GATCCTGAT---GAAGCATGTTTCAGCTGCTGCTGGTTGAGTTACGATCACTTGCACAGC 1295  
Qy 428 HisLeuLysProCysPheLeuTyrLeuSerIlePheProGluAspPheGluIleLysArg 447  
Db 1296 GATCTAAACCATGCTCTTCTGCAATTTTCCAGAAAGCAGTGATATTCAGTG 1355  
Qy 448 AsnArgLeuValGlyArgTrpIleAlaGluGlyPheValArgProLysValGlyMetThr 467

Db 1356 AAGAAATTTGATGAGATCATGATGGCTGAGGGGTTCTCTG-----AAGTTGGAATGAT 1409  
Qy 468 ThrLysAspValGlyGluSerTyrPheAsnGluLeuLeuAsnArgSerMetIle----- 485  
Db 1410 TTGGAAGGAGAGGTTGAGAAAGTGTTCACAAAGACCTTGTGATAGATGTCTAGTCTCGTC 1469  
Qy 486 ---GlnArgSerArgValGlyIleAlaGlyLysThrCysArgIleHisAspIle 504  
Db 1470 ACCAAGAGAGTTCGAGATGGACAC-----AAATTAGATCATGTAAGTTCATGATCTA 1523  
Qy 505 IleArgAspIleThrValSerIleSerArgGlnGluAsnPheValLeuLeuProMetGly 524  
Db 1524 ATATATGACCTGTGCTGAGAGAGTTCAAAGGGAGAACATTTTATCATG----- 1574  
Qy 525 AspGlySerAspLeuVal----- 530  
Db 1575 -----AACGACATGTTCTTGAGCTATCATATCCAGATGTTTCATATCTCTGATGAT 1628  
Qy 531 ---GlnGluAsnThrArgHisIleAlaPheHisGlySerMetSerCysLysThrGlyLeu 549  
Db 1629 AAAATGCAAGCCCTTTAAGCGGTGATGCTGATGATAAATTAATTAATTTGCTCTCAAA 1688  
Qy 550 AspTrpSerIleIle----- 554  
Db 1689 TATAGGCTCTTCTTACCCCTGTAAATCGTTCAGTTGAGAGATCATGACAAACAACTCTT 1748  
Qy 555 -----ArgSerLeuAlaIlePheGlyAspArgProLysSerLeuAlaHisAlaValCys 572  
Db 1749 TTGAAACGAACCCATCTCTCTCTTTTCATCTTGAGCCTTATATATTTATGCTCTCAAA 1808  
Qy 573 ProAsp-----GlnLeuArgMetLeuArgValLeuAspLeuGluAspValThrPheLeu 590  
Db 1809 TCAGAGGTTGTTTCATTTCAAATTAATCAAGTCTTGAGCTGAGA----- 1853  
Qy 591 IleThrGlnLysAspPheAsp-----ArgIleAlaLeuLeuCysHisLeuLys 606  
Db 1854 -----CACAGACAGATTGATGTTTCCCTCGAGAGATACATAAGCCCTCATCTGTTGAGG 1907  
Qy 607 TyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuProArgSerIleGlyLysLeu 626  
Db 1908 TACCTATCATTTG---TTCAGCTATGGAAATTTGATGATCTCCAGAAATTTGCGAGTTA 1964  
Qy 627 GlnGlyLeuGlnThrLeuAsnMetPro-----SerThrTyrIleAlaLeuProSer 644  
Db 1965 TGGAACTCTGCAGACATTCATTTGTTCAAGGTTTCGATCAGATATATAATTTTGTCTGAG 2024  
Qy 645 GluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPheHisTyrAsp 664  
Db 2025 GAAATTTGGAACTAATCAATTAAGCATCTTAA----- 2060  
Qy 665 AsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCysLeuProLysVal 684  
Db 2061 -----CTGCCAGATTT 2072  
Qy 685 PheThrProLeuValSerArgAspArgAlaLysGlnIleAlaGluLeuHisMetAla 704  
Db 2073 TATTTGCCA----- 2081  
Qy 705 ThrLysSerCysTrpSerGluSerIleGlyValLysValProLysGlyIleGly---Lys 723  
Db 2082 -----GATTGCCAAGTGGATCT-----GTTCAAGAGGAGGACTTGGAT 2123  
Qy 724 LeuArgAspLeuGlnValLeuGluTyrValAspIleArgThrSerSerArgAlaIle 743  
Db 2124 TTTTCAAACTTACAAACTATTTCTTACTTGTCTCCAGTTGTCACGAGGAGGTTATTT 2183  
Qy 744 LysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrThrAsnGlySerThr 763  
Db 2184 -----ATGGGG---ATTCAAGATGTCAAAATTAGAATCAGTGGAAATAGGAT--- 2231  
Qy 764 LysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLeuGlnSerLeu 783  
Db 2231 ----- 2231

```
Qy 784 HisValaspalaaglylleserAspGlyGly----- 794
Db 2232 -----GACTATAAAAGTTTTCGGGACTCTGGGCTTCCCAACATCTGTCTATCTGCAG 2285
Qy 795 ThrLeuGluCysLeuaspSerileSerProProLeuLeuLeuAsgThrLeuValLeu 814
Db 2286 CAACCTGGAATATTGAGTCTTATATCTGTGTATATAGCTTTTGCCAGTCAATTTCA 2345
Qy 815 AspGlyLeuLeuGluMetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIle 834
Db 2346 AGTGCA-----AAAGCTTTTCCAGCAAGCTCAGAGAGTTG-----AAAGTTGGAAGAACT 2396
Qy 835 TyrLeuLeuAsgSerLysLeuLysGluGlyLysThrMetLeuLeuLeuGlyAlaLeuPro 854
Db 2397 TATCTAAGCTGTCATCTTGAC-----ATCATAGCTGAGTTGCTT 2438
Qy 855 AsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGlyLys----- 870
Db 2439 AACCTTGAGGTGCTGAAGCTGATGAGCTTGTCTGTGGAAGAAATGGCATCCAATT 2498
Qy 871 -----LeuValPheLys----- 874
Db 2499 GTTATGGGATTAAATCGATTGAAGCTTTTCTTAATAATATAGTTTTCAGTCTCTGG 2558
Qy 875 -----ThrGlyAlaPheProAsnLeuAsgThrLeuTrpIleTyrGluLeuAspGln 891
Db 2559 AAAGCCCAAAATGACAATTTCTGTCTTGAGGCTCATGATTAGAAAGTTGCAAAAT 2618
Qy 892 LeuArgGluLeuAsgPheGluaspGlySerSerProLeuLeuGluLysIleGluIleGly 911
Db 2619 TTGAAGAGATACCCATTGAGTTGAGATATACACACATACAGCTGATGAGTTGAAGA 2678
Qy 912 GluCysArgLeuGluSerGlyIleThrGlyIleLeuHisLeuProLysLeuLysGluIle 931
Db 2679 GAGTGTCT-----CCCAAACTTGGGAATCT 2705
Qy 932 ProIleArgTyrGlySerLysValAlaGlyLeuGlyGlnLeuGluGlyValAlaAsnAla 951
Db 2706 GCTGCAGAGTTCAGAAAGAACAGAACCTCGGA-----AACACCTCTGGGATGT 2759
Qy 952 HisProAsnArgProValLeuLeuMetTyrSerAspArgTyrHis 967
Db 2760 CGTATCTCAATCCATTGAAGGAGAGTGATTTCTGATTGAGAAAGACAT 2807

RESULT 8
US-09-360-186-1
; Sequence 1, Application US/09360186
; Patent No. 6262343
; GENERAL INFORMATION:
; APPLICANT: Staakawicz, et al.
; TITLE OF INVENTION: B2 Resistance Gene
; FILE REFERENCE: 50687
; CURRENT APPLICATION NUMBER: US/09/360,186
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/093,957
; EARLIER FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 31491
; TYPE: DNA
; ORGANISM: Capsicum annuum
US-09-360-186-1

Alignment Scores:
Pred. No.: 7,96e-57 Length: 31491
Score: 614.00 Matches: 250
Percent Similarity: 40.7% Conservativeness: 174
Best Local Similarity: 24.0% Mismatches: 355
Query Match: 11.7% Indels: 264
DB: 3 Gaps: 41
```



; APPLICANT: Staskawicz, Brian J  
 ; APPLICANT: Dahlbeck, Douglas  
 ; APPLICANT: Tai, Thomas H  
 ; FILE OF INVENTION: B62 RESISTANCE GENE  
 ; FILE REFERENCE: 42250/234021 (5830-4A)  
 ; CURRENT APPLICATION NUMBER: US/09/864,680A  
 ; CURRENT FILING DATE: 2001-05-24  
 ; PRIOR APPLICATION NUMBER: US 09/360,186  
 ; PRIOR FILING DATE: 1999-07-23  
 ; PRIOR APPLICATION NUMBER: US 60/093,957  
 ; PRIOR FILING DATE: 1998-07-23  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 31491  
 ; TYPE: DNA  
 ; ORGANISM: Capsicum annuum  
 ; US-09-864-680A-1

Alignment Scores: Pred. No.: 7,96e-57 Length: 31491  
 Score: 614.00 Matches: 250  
 Percent Similarity: 40.7% Conservative: 174  
 Best Local Similarity: 24.0% Mismatches: 355  
 Query Match: 11.7% Indels: 264  
 DB: 3 Gaps: 41

US-10-656-394A-8 (1-1032) x US-09-864-680A-1 (1-31491)

Qy 34 ValGluLysAspIleTrpTyrIleLysAspGluLeuLysThrMetGlnAlaPheLeuArg 53  
 Db 1447 GTCCGAAGGAC-----AAAACGAGAAATCAGTATATATGGCTCATGCAAGT 1494  
 Qy 54 AlaAlaGluLeuMetLysLysAspGluLeuLysValTrpAlaGluGlnIleArg 73  
 Db 1495 GTGGCTCTCTTATGAGAACATAGATCTCTCTG--ACATTCAATTCGCGGATGCAA 1551  
 Qy 74 AspLeuSerTyrAspIleGluAspSerLeuAspGluPheLysValHisLeuGlnSerGln 93  
 Db 1552 TCTATCTCTGATGACAGAGAACTTTGCGCTCTCGTGAAGTTAGTTCCTCG 1611  
 Qy 94 ThrLeuPheArgGlnLeuValLysLeuArgGluArgHisArgIleAlaIleArgIleHis 113  
 Db 1612 GAAGTATTT-----GTCAAGAACTTTGAGAAACAAATGTTTGGGGAATGACG 1662  
 Qy 114 AsnLeuLysSerArgValGluGluValSerSer----- 124  
 Db 1663 GATTTTGAAGTAGAGGTAAAGAGAGTTGCAAGTCTGCTGAATACAAATTCAACTGAGA 1722  
 Qy 125 ----- 127  
 Db 1723 CTAACAGGAACGTGACTGGGAGAAATAAAGCCAGAAAAAGGCGGTGCAAGTTT 1782  
 Qy 128 ArgTyrSerLeu-----ValLys 133  
 Db 1783 CGTCAAGGCTGCAACAAAGTACGAGGACATGATCATATCTCGAAGAGTGCACAAAG 1842  
 Qy 134 ProIleSerSerGlyThrGluIleAspMetAspSerTyrAlaGluAspIleArgAsnGln 153  
 Db 1843 ATCCAGATAAAGGAAACAAAGTATCAAGGAATCATTTGTTTCATGATTTT---TCAAGT 1899  
 Qy 154 SerAlaArgAsnValAspGluAlaGlu-----LeuValGlyPheSerAspSerLysLys 171  
 Db 1900 TCAACAAACGATATTTGAAGGTTAAGAACAAATATGTTGGACGTGATGATCAAAAGGAAA 1959  
 Qy 172 ArgLeuLeuGluMetIleAspThrAsnAlaAsnAspGlyProAlaLysValIleCysVal 191  
 Db 1960 CAGTTGTTAAGACATCTG---ACTAGAGCTACTCTGGGAACCCAAAGTCAATCCCGATT 2016  
 Qy 192 ValGlyMetGlyGluGlyThrAlaLeuSerArgLysIlePheGluSerGluGlu 211  
 Db 2017 GTCGGATGGGAGGATAGGTAAACCAACCTTAGCAAAAGAGTTTAC---AATGATGAA 2073

Qy 212 AspIleArgLysAsnPheProCysAsnAlaTrpIleThrValSerGlnSerPheHisArg 231  
 Db 2074 TCAATTTCTATGCGGTTTGTATGCTGCTGGGCTACCATATATCAACAGCACAACAA 2133  
 Qy 232 IleGluLeuLysAspMetIleArgGlnLeuGlyProSerSerLeuAspGlnLeu 251  
 Db 2134 AAGGAAATTTGCTGGGCTTCTGCATTCACAAATCAAAATGATGATGAGGTTAAGATG 2193  
 Qy 252 LeuGlnGluLeuGlnGlyLysValValGlnValHisLeuSerGluTyrLeuIle 271  
 Db 2194 ATTGGTGAAGCAGAG-----CTAGCAGACATGTTTACAG 2226  
 Qy 272 GluGluLeuLysGluLysArgTyrPheValValLeuAspAspLeuTrpIleLeuHisAsp 291  
 Db 2227 AAAAGTTTAAAGAGAAAGAGGTACTTAATTTGTTCTGGATGATATCTGGAGTTGTGAGTG 2286  
 Qy 292 TrpAsnTrpIleAsnGluIleAlaPheProLysAsnAsnLysLysGlySerArgIleVal 311  
 Db 2287 TGGGATGGCTCAGACGA--TGCTTTCCAACTCAAGACAAATCGAGGAGTCCAAATCTG 2343  
 Qy 312 IleThrThrArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeuValTyrHis 331  
 Db 2344 TTGACTACCGTATGATGAGTAGCTTGTATGCTGCTGAGAGATTTTCTTTGCGG 2403  
 Qy 332 LeuAspPheLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArgLysThrAsnLysAsn 351  
 Db 2404 ATGAGCTTTCATGGATCAAGATGAGATTGGAGT---CTTTTCAAAAGTGCAGCATTTTCA 2460  
 Qy 352 HisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIleValAsnLys 371  
 Db 2461 AGTGAAGCATTACCA-----TATGATTCGAGACTGTTGGAAAGCAATCCAGATGAA 2514  
 Qy 372 CysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrLysGln--- 390  
 Db 2515 TGTCAAGGTTTACCACATACTATTGCTGCTGGTGCAGGCTCTCAAAATCTAAAGGACA 2574  
 Qy 391 ValSerGluTrpGluLysPheTyrGluHisLeuProSerGluLeuLeuLeuAsnProSer 410  
 Db 2575 ATAGAAGATTGGAATACTGTTGCTAAAGATGTCAAGTCAATCTGTCACAAATGATCCTGAT 2634  
 Qy 411 LeuGluAlaLeuArgArgMetValThrLeuGlyTyrAsnHisLeuProSerHisLeuLys 430  
 Db 2635 --GAACGATCTTCACGTGCTGCTGGTGGTTCAGTACATCTGCAAGCGCATCTAAA 2691  
 Qy 431 ProCysPheLeuTyrLeuSerIlePheProGluAspPheGluIleLysArgAsnArgLeu 450  
 Db 2692 ACATGCTCTCTGCAATTTGGAATTTTCCAGAGACAGTGATATTCAGTGAAGAAATTG 2751  
 Qy 451 ValGlyArgTrpIleAlaGluGlyPheValArgProLysValGlyMetThrThrLysAsp 470  
 Db 2752 ATGAGATCATGATGCTGAGGGGTTCTCTG-----AGTTGGAATAATGATTTGGAAGA 2805  
 Qy 471 ValGlyGluSerTyrPheAsnGluLeuIleAsnArgSerMetIle-----GlnArg 487  
 Db 2806 GAGGTTGAGAAGTGTTCGAAGAGCTGTGCTAGATGATGCTAGTCTCTGCTCAGCAAGA 2865  
 Qy 488 SerArgValGlyIleAlaGlyLysIleLysThrCysArgIleHisAspIleIleArgAsp 507  
 Db 2866 AGTCGAGATGGAACA-----AAATATAGATCATGTAAGTTTCATGATCTAATATGAC 2919  
 Qy 508 IleThrValSerIleSerArgGlnGluAsnPheValLeuLeuProMetGlyAspGlySer 527  
 Db 2920 CTGTGCTGAGAGAGTTCAAAGGGAGAACATTTTTTATCATG-----AAC 2964  
 Qy 528 AspLeuVal-----GlnGlu 532  
 Db 2965 GACATTTGTTCTGAGCTATCATATCCAGATGTTCTCATCTCTGTATGATATAAATGAG 3024  
 Qy 533 AsnThrArgHisIleAlaPheHisGlySerMetSerCysLeuThrGlyLeuAspTrpSer 552  
 Db 3025 CCCTTTAAGCGCGTGAAGTGTGATGAAATTAATTTATTTGTCCTTATGTTGCTTTTATAGG 3084  
 Qy 553 IleIle-----Arg 555

Db 3085 CTTCTTACCCCTGTAATTCGTCAGTTCAGAGATCATGACACAAACAATCTTTTGAACGA 3144  
Qy 556 SerLeuAlaIlePheGlyAspArgProLysSerLeuAlaHisAlaValCysProAsp--- 574  
Db 3145 ACCATCTCTGTTCTCTTTTCATCTTGAGCCTTTATATTATGTTCTCAATCAGAGTT 3204  
Qy 575 ---GlnLeuArgMetLeuArgValLeuAspLeuGluAspValThrPheLeuIleThrGln 593  
Db 3205 GTTCATTTCAATTAATCAAGTCTTGAGCTGAGA-----CAC 3243  
Qy 594 LysAspPheAsp-----ArgIleAlaLeuLeuCysHisLeuLysTyrLeuSer 609  
Db 3244 AGACAGATTGATGTTTCCCTCGAGAGATCACTAAGCCTCATCTGTTGAGGTACCTATCA 3303  
Qy 610 IleGlyTyrSerSerIleTyrSerLeuProArgSerIleGlyLysLeuGlnGlyLeu 629  
Db 3304 TTG---TTCAGCTATGGGAATTTTCGATGTACCTCCAGAAATTTGCAGGTTATGGAATCTG 3360  
Qy 630 GlnThrLeuAsnMetPro-----SerThrTyrIleAlaAlaLeuProSerGluIleSer 647  
Db 3361 CAGACATTCATTTGTCACGGTTTCGATCAGATATATAATTTTCTGAGGAATTTGG 3420  
Qy 648 LysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPheHisTyrAspAsnPheSer 667  
Db 3421 GAACTAATGCAATTAAGCATCTTAAA----- 3447  
Qy 668 LeuAsnHisProMetLysCysIleThrAsnThrIleCysLeuProLysValPheThrPro 687  
Db 3448 -----CTGCCAGATTTTATTGGCA 3468  
Qy 688 LeuValSerArgAspArgAlaLysGlnIleAlaGluLeuHisMetAlaThrLysSer 707  
Db 3469 -----GAT 3471  
Qy 708 CysTrpSerGluSerIleGlyValLysValProLysGlyIleGly---LysLeuArgAsp 726  
Db 3472 TGCCCAAGTGGATCT-----GTTGACAAAGAGAGGCACTTGGATTTTCAAC 3519  
Qy 727 LeuGlnValLeuGluTyrValAspIleArgThrSerArgAlaIleLysGluLeu 746  
Db 3520 TTACAACTATTTCTTACTTGTCTCCAGTTGTTGCACGAAGGAGGTATT-----ATG 3573  
Qy 747 GlyGlnLeuSerLysLeuArgLysLeuGlyValThrThrGlnGlySerThrLysGluLys 766  
Db 3574 GGG---ATTGAGAAATGTCAAAATTTAGAAATCAGTGAATTAAGGAT----- 3618  
Qy 767 CysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLeuGlnSerLeuHisValAsp 786  
Db 3619 -----GAC 3621  
Qy 787 AlaAlaGlyIleSerAspGlyGly-----ThrLeuGlu 797  
Db 3622 TATAAAGTTTTCGGGACTCTGGGCTTCCCAACAATCTTGTCTATCTGACGCACTTGAA 3681  
Qy 798 CysLeuAspSerIleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIle 817  
Db 3682 ATATTGAGCTTATATCTGTTGATTATAGCTTTTTCAGTGTATCATTTCAAGTGA--- 3738  
Qy 818 LeuGluLysMetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeu 837  
Db 3739 ---AAAGCTTTTCCAGCAACGCTCAAGAAAGTTG---AAGTTGGAAGAACTATCTAAGC 3792  
Qy 838 ArgSerLysLysGluGlyLysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMet 857  
Db 3793 TGTCATCTTGGAC-----ATCATAGCTGAGTTGCTTAACCTTGAG 3834  
Qy 858 ValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLys----- 870  
Db 3835 GTCTGAAGCTATGATGACGCTTGTGTGTGAGAAATGGCATCCAAATGTTATTATGGGA 3894  
Qy 871 -----LeuValPheLys----- 874

Db 3895 TTTAATCGATTGAAGCTTTTCTTAATTAATATAGTTTCTCAAGTTCTGGAAGCCACA 3954  
Qy 875 ThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyrGluLeuAspGlnLeuArgGlu 894  
Db 3955 AATGCAATTTTCTGCTTTCAGCCCTCATGATTAGAGTTGCAAAATTTGAAGAG 4014  
Qy 895 IleArgPheGluAspGlySerSerProLeuLeuGluLysIleGluIleGlyGluCysArg 914  
Db 4015 ATACCATTTGATTTGCAGATATACACACTACACTGATTGAGTTAAGAGAGTGTCT 4074  
Qy 915 LeuGluSerGlyIleThrGlyIleLeuHisLeuProLysLeuLysGluIleProLeuArg 934  
Db 4075 -----CCCAAACTTGGGAATTTCTGTCACGA 4101  
Qy 935 TyrGlySerLysValAlaGlyLeuGlyGlnLeuGluGlyGluValAsnAlaHisProAsn 954  
Db 4102 ATTCAAAAGAACAGAGAGACCTCGA-----AAC 4131  
Qy 955 ArgProVal 957  
Db 4132 AACCCCTGTG 4140

RESULT 10  
US-09-360-186-4  
; Sequence 4, Application US/09360186  
; Patent No. 6262343  
; GENERAL INFORMATION:  
; APPLICANT: Staskawicz, et al.  
; TITLE OF INVENTION: B2 Resistance Gene  
; FILE REFERENCE: 50687  
; CURRENT APPLICATION NUMBER: US/09/360,186  
; CURRENT FILING DATE: 1999-07-23  
; EARLIER APPLICATION NUMBER: 60/093,957  
; EARLIER FILING DATE: 1998-07-23  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 2718  
; TYPE: DNA  
; ORGANISM: Capsicum annuum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2718)  
US-09-360-186-4

Alignment Scores:  
Pred. No.: 3,1e-58 Length: 2718  
Score: 609.50 Matches: 243  
Percent Similarity: 42.7% Conserved: 188  
Best Local Similarity: 24.1% Mismatches: 361  
Query Match: 11.6% Indels: 219  
DB: 3 Gaps: 40

US-10-656-394A-8 (1-1032) x US-09-360-186-4 (1-2718)

Qy 42 LysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaGluLeuMetLysLysLys 61  
Db 91 AGAGAAGAACTTTCGCTCTTCGTGAAAAAAGTTAGTTCCCTGGAAGTATTGTCAGAAC 150  
Qy 62 AspGluLeuLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGluAsp 81  
Db 151 TTTGAAAAACAATGTTTTTGGGAA---ATACCGATTTTCAAGTAGAGTAAGAA 207  
Qy 82 -----SerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeu 99  
Db 208 GTTGAAGTGTCTGTAATCACAATTCAGACTACAGAACTGTCTGCGGAA 267  
Qy 99 uValLysLeuArgGluArgHisArgIleAla-----IleArgIleHisLeuLysSe 117  
Db 268 ATAAAGCCAGAAAAAAGCGCGTTCGAGAGTTTCGTCAAGCTTCGACAAAGTAGCA 327  
Qy 117 rArgValGluGluValSerSerArgAsnThrArgTyrSerLeuValLysProIleSerSe 137







394 pGLuLysPheTyGluHiLsLeuProSerGluLeuGluLeuLeuAenProSerLeuGluLaLe 414  
 1107 GAAAACTGTTGCTAAAGATGCTCAAGTCATTCTGCTCAAAATGATCTCTGAT--GAACGATG 1163  
 414 uAArgMetValThrLeuGlyTyAenHisLeuProSerHisLeuLysProCysPheLe 434  
 1164 TTCAGCTGTGCTTGGTTGAGTTACGATCACTTGACACGGATCTAAAACATGCTCTCT 1223  
 434 uTyLeuSerllePheProGluAapPheGluLlleLysArgAenArgLeuValGlyArgTr 454  
 1224 GCATTCGGAATTTTTCAGAAGACAGTGAATTCAGTGGAAGATTTGATGAGATCATG 1283  
 454 pIleAlaGluGlyPheValArgProLysValGlyMetThrThrLysAspValGlyGluSe 474  
 1284 GATGCTCAGGGGTTCTCTG-----AAGTTGGAATAATGATTTGGGAAGCAGAGGTTGAA 1337  
 474 rTyPheAenGluLeuLeuAenArgSerMetlle-----GlnArgSerArgValG 491  
 1338 GTGTTTGCAGAGCTTTGCGATAGATCTAGTCCTCTGCACAGAAGAGTCGAGATG 1397  
 491 yIleAlaGlyLyslleYsthrCysArglleHisAspIlelleArgAspIleThrValSe 511  
 1398 AACA-----AAAATTAGATCATGTAAGGTTTCATGATCTAATATATGACCTGTGCGTGAG 1451  
 511 rIleSerArgGlnGluAenPheValLeuLeuProMetGlyAspGlySerAspLeuVal-- 530  
 1452 AGAAGTTCAAAGGGGAACAATTTTATCATG-----AACGACATGTTCT 1496  
 531 -----GlnGluAenThrArgHi 536  
 1497 TGACGTATCATATCCAGAATGTTCATATCTCTGATGATATAAAATCGACGCCCTTAAAGCG 1556  
 536 sIleAlaPheHisGlySerMetSerCysLysThrGlyLeuAapTrpSerllelle----- 554  
 1557 CGTGACTGGTGATGAATAATTAATTTGCTCCTATGTCCTTAAGGCTCTCTTACCCC 1616  
 555 -----ArgSerLeuAlaI 559  
 1617 TGTAAATCGTCAGTTCAGAGATCATGACACAAACAATCTTTTGAACACGAACCCATCTGT 1676  
 559 ePheGlyAspArgProLysSerLeuAlaHisAlaValCysProAsp-----GlnLeuAr 577  
 1677 TTTCCTTTTCATCTTGAGCCCTTATATATGTTCTCAAAATCAGAGGTTGTTCAATTCAA 1736  
 577 gMetLeuArgValLeuAspLeuGluAapValThrPheLeulleThrGlnLysAspPheAs 597  
 1737 ATTACTCAAAGTCTTGGAGCTGACA-----CACAGACAGATGTA 1775  
 597 p-----ArglleAlaLeuLeuCysHisLeuLysTyLeuSerlleGlyTyIse 613  
 1776 TGGTTTCCTCGAGATACTAAGCCTCATCTGGTTGAGTACCTATCATG--TTTCAG 1832  
 613 rSerSerlleTySerLeuProArgSerlleGlyLysLeuGlnGlyLeuGlnThrLeuAs 633  
 1833 CTATGGGAATTTTCGATGTACCTCCAGAAATTTTCAGGTTATCGAATCTGCAGACATTCAT 1892  
 633 nMetPro-----SerThrTyrlleAlaAlaLeuProSerGluLleSerLysLeuGlnCy 651  
 1893 TGTTCAACGGTTTCGATCAGATATAATAATTTTGTGAGGAAATTTGGGAACCTAATGCA 1952  
 651 sIleuHisThrLeuArgCyslleGlyGlnPheHisTyAenPheSerLeuAenHisPr 671  
 1953 ATTAAGGCATCTTAA----- 1968  
 671 oMetLysCyslleThrAenThrIleCysLeuProLysValPheThrProLeuValSerAr 691  
 1969 -----CTGCCCAAGATTTTATTTGCA----- 1989  
 691 gAspAspArgAlaLysGlnlleAlaGluLeuHisMetAlaThrLysSerCysTrpSerGl 711  
 1990 -----GATTCGCCCAAGTGG 2003  
 711 uSerlleGlyValLysValProLysGlylleGlyLysLeuArgAspLeuGlnValle 730

RESULT 12

RESULT 12  
US-08-930-996A-3

US-08-550-550A-3  
: Sequence 3, Application US/08930996A

Patent No. 6100449

GENERAL INFORMATION:

APPLICANT: FLUHR, Robert

APPLICANT: ESHED, Yuval

APPLICANT: ORI, Naomi

APPLICANT: PARAN, ilan

APPLICANT: ZAMIR, Daniel

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
84

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/930.996A  
 FILING DATE: 09-DEC-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/05272  
 FILING DATE: 15-APR-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: IL 113.373  
 FILING DATE: 13-APR-1995  
 INFORMATION FOR SEQ ID NO. 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4465 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 204...3923  
 US-08-930-996A-3

Alignment Scores:  
 Pred. No.: 1,28e-57 Length: 4465  
 Score: 607.50 Matches: 249  
 Percent Similarity: 41.9% Conservative: 183  
 Best Local Similarity: 24.2% Mismatches: 388  
 Query Match: 11.5% Indels: 211  
 DB: 3 Gaps: 42

US-10-656-394A-8 (1-1032) x US-08-930-996A-3 (1-4465)

Qy 3 GluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAlaAlaSer 22  
 Db 207 GAGATTGGCTTACGAGTTGGTGGTGCATTCTCTCCTCAGCTTGAATGCTTGTGAT 266  
 Qy 23 AlaAlaAlaAspGluThrSerLeuLeuLeuGlyValGluLysAspIleTrpTyrIleLys 42  
 Db 267 AGGCTTGCTCTCAACGGTGATCTGCTCAACATGTTTCGGAAGCATAGGATCATGTTAAG 326  
 Qy 43 AspGluLeuLysThrMetClnAlaPheLeuArgAlaAlaGluLeuMetLysLysLysAsp 62  
 Db 327 ---CTCTTAAGAAGCTGAAATGATCTTGGCGGTATTCAGATTGTGCTAAGTATGCA 383  
 Qy 63 GluLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGluAspSer 82  
 Db 384 GAGAATAAGCAAGCATCAATCCATCTGTGAGAGACTGGCTTAATGAGCTTCGAGATGCT 443  
 Qy 83 LeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuValLysLeu 102  
 Db 444 GTGCACTCTGCTGAAATTTAATAGAAGCACTTCAATTAATGAGCTTTGAGGCTTAAGGTG 503  
 Qy 103 ArgGluArgHisArgIleAlaIleArgIleHisAsn----- 114  
 Db 504 GAAGGTCAGCATCAGACACTTTTCAGAAACCAAGCAACGACGAGTAAAGTATGATGATTTTC 563  
 Qy 115 -----LeuLysSerArgValGluGluValSerSerArgSerThrArg 128  
 Db 564 CTTAACAATAAGCAAGTTGGAAGACACTATTGAACATTAAAGGATTTGCAAGACAA 623  
 Qy 129 TyrSerLeuValLysProIleSerSerGlyThrGluIleAspMetAspSerTyrAlaGlu 148

Db 624 ATTGGTCTCCTT-----GGCTTAAAGGAGTATTTCATTCCACGAACTA 668  
 Qy 149 AspIleArgAsnGlnSerAlaArgAsnValAspGluAlaGluLeuValGlyPheSerAsp 168  
 Db 669 GAACTAGAACACCTTCAACTCTTTGATGATGAACACGATATCTTTGGT----- 719  
 Qy 169 SerLysLysArgLeuLeuGluMetIleAspThrAsnAlaAsnAspGlyProAla----- 186  
 Db 720 AGGAGAGCGAANTAGAGGATTGATGACCGTCTATTGCTGAAGGTCAAGTGGGAA 779  
 Qy 187 -----LysValIleCysValValGlyMetGlyGlyLeuGlyLysThrAlaLeuSerArg 204  
 Db 780 AATCTGACAGTGGTCTTATTGTTGGAATGGGTGGCTTGGGCAAGCAACACTTGTCTAAA 839  
 Qy 205 LysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsnAlaIleThr 224  
 Db 840 GCCGTATAC---AATGATGAGAGTGTGAAGAACATTTGATTGGAAGCTTGGTTTGT 896  
 Qy 225 ValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArgGlnLeuGly 244  
 Db 897 GTTTCGAGCGGTATATGCTTTTCAGAAATAACAAAGGGTTACTTCAAGAAATTTGCTCA 956  
 Qy 245 ProSerSerLeuAspGlnLeuGlnGluLeuGlnGlyLysValValGlnValHis 264  
 Db 957 ATTGACTTAGTTGATGACATCTTAATCACTACAGTCAAA----- 998  
 Qy 265 HisLeuSerGluTyrLeuIleGluGluLysGlyLysArgTyrPheValValLeuAsp 284  
 Db 999 -----TTGAAGGAAGATTAAGGAAAGAAAGTTCTTATCGTCTCGAT 1043  
 Qy 285 AspLeuTrp-----IleLeuHisAspTrpAsnTrpIleAsnGluLeuAlaPheProLys 302  
 Db 1044 GATGTGGAATGACAACTACAGAGTGGGATTTGAGAAATGTTTGTGA----- 1097  
 Qy 303 AsnAsnLysLysGlySerArgIleValIleThrThrArgAsnValAspLeuAlaGluLys 322  
 Db 1098 CAAGGAGATATAGGAAGTAAAGATCATTTGTGACGACGCAAGACAGAGTGTGCTGTATG 1157  
 Qy 323 CysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAspAlaIleThr 342  
 Db 1158 ATGGGAATGAGCAAAATF-----AGCATGGGCAATTTGTCTACCGAAGCCTTGGTCT 1211  
 Qy 343 LeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsnMetGln 362  
 Db 1212 TTATTTCAAGACATGATGCTTGAAGAAACATGATGCTCTATG---GGACATTGGGAACCTGAA 1268  
 Qy 363 LysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeuThrIle 382  
 Db 1269 GAGGTGGAAGCAAAATGCGAGCTAAGTGAAGGAGCTGCCCTTAGCTCTGAAGACGCTT 1328  
 Qy 383 GlyAlaValLeuAlaThrLys---GlnValSerGluTrpGluLysPheTyrGluHisLeu 401  
 Db 1329 GCTGGCATGTTACGCTCCAAATCAGAGTTGAAGAGTGGAAATGATTTCTGAGAAGTGA 1388  
 Qy 402 ProSerGluLeuGluIleAsnProSerLysLeuAlaLeuArgMetValThrLeuGly 421  
 Db 1389 ATATGGAGCTCGGAGACATGATGATATACAGCGTTA-----ATGTTGAC 1436  
 Qy 422 TyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePheProGlu 441  
 Db 1437 TACATGATCTCTCGACATTTAAGCGATGCTTTCTTTTGTGCAATATTTCTTAAA 1496  
 Qy 442 AspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheValArg 461  
 Db 1497 GATTATCATTTTAGGAAAGAACAAAGTTATTTCATCTATGATTTGCCATGCTCTTTGA--- 1553  
 Qy 462 ProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeuLeuAsn 481  
 Db 1554 CTTGTGGAAGATGAATAATTCAGATTTAGGCAACCAATTTCTTCTCGAGTTGAGTTCA 1613  
 Qy 482 ArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCys---Arg 500  
 Db 1614 AGATCATTTATTGAAGGGTCCCAATCTTCTGAGGAAACATAAAGGAATTTATTCCTA 1673

Qy	827	GlnLeuThrHisLeuLysLysIleTyLeuLeuArgSerLysLeuLysGluGlyLysThr	846
Db	2529	GATCTTTGTTCTTAAGCTGGTGAATTTGTCTCTTAGAACTGCAAGGACTGTTACTCC	2588
Qy	847	MetLeuIleLeuGlyAlaLeuProAsnLeuMetValLeuHisLeuTyArgAsnAlaTy	866
Db	2589	TGCGCAGCACTAGGACAACTCCCTTGTGTGAATTCCTTCCGTT-----AAGGGGATG	2642
Qy	867	LeuGlyGluLysLeuValPheLysThr-----GlyAlaPheProAsnLeuArgThrLeu	884
Db	2643	CATGGAATAAGAGTGGTGACGGAAGAAATTCACGGCAGATTGTCTCTCAAAAAG-----	2696
Qy	885	TrpIleTyGluLeuAspGlnLeuArgGluIleArgPheGluAsp-----	899
Db	2697	-----CCTTTTAACTGCTCTTGAAAGCTTGAATTTGAAGATATGACAGAGTGGAG	2747
Qy	900	-----GlySerSerProLeuLeuGluLysIleGluIleGlyGlu	912
Db	2748	CAATGGCCAGCAGCTAGGAAATTGGAGAGTTCCCTACACTTGAGAAGCTTCAATTATAAAT	2807
Qy	913	CysArgLeuGluSerGlyIleThrGlyIleIleHisLeuProLysLeuLys-----GluIle	931
Db	2808	TGC-----CCTGAGCTCAGTTGGGAGATA	2831
Qy	932	ProIleArgTyGlySer-----LysValAlaGlyLeu-----	942
Db	2832	CCGATCCAAATTTCAAGTTTAAAGAGTTTAGGGTTTTGGTTGTCCAGTTGTTTTTAT	2891
Qy	943	-----GlyGlnLeuGluGly	947
Db	2892	GATGCTCAAGTGTTAAGATCCCAACTTGAGGA	2924

REF ID: A63011 13  
US-09-004-838-1

US-09-004-838-1  
Sequence 1, Application US/09004838  
Patent No. 6350933  
GENERAL INFORMATION:  
APPLICANT: Michelmore, Richard W.  
APPLICANT: Shen, Kathy  
APPLICANT: Meyers, Blake  
TITLE OF INVENTION: Procedures and Materials for  
TITLE OF INVENTION: Conferring Pest Resistance in Plants  
NUMBER OF SEQUENCES: 140  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/004,838  
FILING DATE: 09-JAN-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/781,734  
FILING DATE: 10-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Einhorn, Gregory P.  
REGISTRATION NUMBER: 38,440  
REFERENCE/POCKET NUMBER: 023070-078810US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4208 base pairs  
TYPE: nucleic acid





QY	570	AlaValCysProAspGlnLeuArg-----MetLeuArgValLeuAspLeuGluAsp	586
DB	2806	AAGGCTTTGAATGACWTACTTACCAATGTTTAAGGGTCTCTRAKTTTG-----	2859
QY	587	ValThrPheLeuIleThrGlnLysAspPheAspArgIleAlaLeuLeuCysHisLeuLys	606
DB	2860	-----ATTRRTCTT-----	2868
QY	607	TyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuProArgSerIleGlyLysLeu	626
DB	2869	-----AVAAATRAVRAGGTACCARAATCGTSGGTATGATG	2904
QY	627	GlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAlaAlaLeuProSerGluIle	646
DB	2905	AASCACTTGGCGTATCTTAATCTATCWGRAACTTAAATCACMCATTTACCGGAATKTC	2964
QY	647	SerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPheHisTyrAspAsnPhe	666
DB	2965	TGCATCTTTAATTTACARACCTGATGTGKTCGTGTGAMTAT-----	3012
QY	667	SerLeuAsnHisProMetLysCysIleThrAsnThrIleCysLeuProLysValPheThr	686
DB	3013	-----TTAGTTAAKTTGTCCTCCCAACACCTCTCTCA	3039
QY	687	ProLeuValSerArgAspArgAlaLysGlnIleAlaGluLeuHisMetAlaThrLys	706
DB	3040	AASCTT-----AAAATTTGCASCATTTCAGTCAGGGGTACT	3078
QY	707	SerCysTrpSerGluSerIleGlyValLysValProLysGlyIleGlyLysLeuArgAsp	726
DB	3079	CKAAKTTTAAAR-----AACTATGCCCTTARGGATTTGGTGARTTGGAAART	3123
QY	727	LeuGlnValLeu---GluTyrValAspIleArgArgThrSerSerArgAlaIleLysGlu	745
DB	3124	CTACAAACTCTCTTVMGTAACTTGCATAGCAATAACCGAGCTTAAAGAACTTCMAAY	3183
QY	746	Leu-----GlyGlnLeuSerLysLeuArgLys---LeuGlyValThr	758
DB	3184	CTCCATGGGAARTTTGATTTGCGCGCTGGGAAAAATGGAAATGCMGTGKGATGCACG	3243
QY	759	ThrAsnGlySerThrLysGluLys-----	766
DB	3244	TTAAGCGCAACTGTCTCAAAAAAGGTTAAATGARTTANAACTGGRWTKGGGGGTGATRA	3303
QY	767	-----CysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLeuGlnSerLeuHis	784
DB	3304	ATTAAATGTTTCGGAATCGGAACACTTGAAGAAAGTCTCTCAATGAG-----	3354
QY	785	ValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLeuAspSerIleSerSer	804
DB	3355	-----TGATGCCTCATATGATCTACTCTAN	3378
QY	805	ProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGluGluMetProAsnTrp	824
DB	3379	AAAAAACCCANAAT-----ATGCTCTATAGGGGTATA-----GAGTTCCAAATTTG	3426
QY	825	IleGluGlnLeuThrHisLeu-----LysLysIle	834
DB	3427	GTGTGGTNCACATAAGGGTTCTGAAACTAGAGATGTGTTTCATGGTGTATGAAAAAGANTG	3486
QY	835	TyrLeuLeuArgSerLysLeuLysGlu-GlyLysThrMetLeuIleLeuGlyAlaLeuPr	854
DB	3487	TTTTACGTAGTTTTCATCAATCAACCAAGTGGGAAATAGATGATATTTTCAGGCGCTACTGA	3546
QY	854	oAsnLeu-----MetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLysLe	871
DB	3547	TGAGATGTGGAGAGGTATGATA-----GGGTWCTTTGGGCGGTAGA	3588
QY	871	uValPheLysThrGlyAlaPheProAsnLeuLeuArgThrLeuTrpIleTyrGluLeuAspGI	891
DB	3589	AGAAATAGCATCACTTTGTAATGAAATAAGATATTTGTGGGAATCAGAAGCAGAGGC	3648

```

Qy 891 nleuArgGluIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGluIleG1 911
Db 3649 AAGTAAGGTTCTTATG-----AATTTAAAGAGTTGGATTAGG 3687
Qy 911 yLcUcYArgLeuGluSerGlyIleIleHisLeuProLysLeuLysGlu 930
Db 3688 TGAATGTGAA-----AATTGCTGAGTTTAGCGGAGAAAAGGAG 3727

RESULT 14
US-09-004-838-70
; Sequence 70, Application US/09004838
; Patent No. 6350933
; GENERAL INFORMATION:
; APPLICANT: Michelmore, Richard W.
; APPLICANT: Shen, Kathy
; APPLICANT: Meyers, Blake
; TITLE OF INVENTION: Procedures and Materials for
; TITLE OF INVENTION: Conferring Pest Resistance in Plants
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/004,838
; FILING DATE: 09-JAN-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/781,734
; FILING DATE: 10-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Einhorn, Gregory P.
; REGISTRATION NUMBER: 38,440
; REFERENCE/DOCKET NUMBER: 023070-078810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4163 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..4163
; OTHER INFORMATION: /note= "RLGI-E169"
US-09-004-838-70

Alignment Scores:
Pred. No.: 3 43e-56 Length: 4163
Score: 594.50 Matches: 265
Percent Similarity: 39.5% Conservative: 187
Best Local Similarity: 23.1% Mismatches: 373
Query Match: 11.3% Indels: 320
DB: 3 Gaps: 48

US-10-656-394A-8 (1-1032) x US-09-004-838-70 (1-4163)

Qy 1 MetAlaGluThrValIleuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20
Db 1099 ATGCTGAATCGTCTTCTTCGCTCTTTCAGTCAGTGGTG-----TTTGAAGAAGCTG 1149
Qy 21 AlaSerAlaAlaAlaAspGluThrSerLeuLeuGlyValGluLysAspIleTrpTyr 40

```

2125	Db	2125	GGTGATCAACAACTTTGATTGATCCATCCACCACTAAAGGCCCATGGAGCACTGTTGTGTGAAG	2186
371	Qy	371	LysCysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrLysGln	390
2185	Db	2185	AAATGTGATGCTTTACCTCTAGCYTTTAAAGAACACTTTGGAAGGTTATTAAAGCACAAA	2241
391	Qy	391	ValSerGluTyrGluLysPheTyrGluHisLeuProSerGluLeu	405
2242	Db	2242	---ACAGACAGGAGAACAACTGGAAGGAGCTTTGGATAGTGAGATCGAGGTTAGGAAG	2298
406	Qy	406	-----GluIleAsnProSerLeuGluAlaLeuArgArgMetValThrLeuGlyTyrAsn	423
2299	Db	2299	AGCGATGAGATTGTTCCGGCTCTTGA	2337
424	Qy	424	HisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePheProGluAspPhe	443
2338	Db	2338	GATCTTTCTGCCCTTTGAAGCTRTTTRTTTGGCATATGCTCTCTGTTTCCCAAGGACTAT	2397
444	Qy	444	GluIleLysArgAsnArgLeuValGlyArgTyrIleAlaGluGlyPheVal	462
2398	Db	2398	GAGTTTGACAGGAGGAGTTGATCTATTGTTGGATGGCAGAGGGTTTTTCCACCAACCA	2457
463	Qy	463	LysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeuIleAsnArg	482
2458	Db	2458	ACTAATAACAAGTCAAAGCAACGKTGGGCTTGTAATATTTTAAAGAGTTTCTGTCAGR	2517
483	Qy	483	SerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArgIle	501
2518	Db	2518	TCRTTTTTCAACAT	2562
502	Qy	502	HisAspIleIleArgAspIleThr	511
2563	Db	2563	CATGACCTATTGAATGATTGGCTACATTTGTTGCTGGAGAATTTTTTCAAGGTTAGAC	2622
512	Qy	512	IleSerArgGlnGluAsnPheValLeuLeuProMetGlyAspGlySerAspLeuValGln	531
2623	Db	2623	ATAGAGATGACAGAGGAATTTAGATGSAATCTTTG	2658
532	Qy	532	GluAsnThrArgHisIleAla	538
2659	Db	2659	GARAAGCACCCGWCATATGTCATTTGATGTGAGRATTACATAGGTTACAAAARGTTTCGAG	2718
539	Qy	539	---PheHisGlySerMetSerCysLysThrGlyLeu	549
2719	Db	2719	CAATTTAGAGAGCTAAAATTTGAGAACATTTTAGCATGCTCTGTTGGGGTGGTAGAA	2778
550	Qy	550	AspTyrSerIleIleArgSerLeuAlaIlePheGlyAspArgProLysSerLeuAlaHis	569
2779	Db	2779	GATTGGAAGATGTTT	2805
570	Qy	570	AlaValCysProAspGlnLeuArg	586
2806	Db	2806	AGGCTCTGGAATGACWTACTCTCARGATTTTACCATTGTTAAGGCTCTRAKTTTG	2859
587	Qy	587	ValThrPheLeuIleThrGlnLysAspPheAspArgIleAlaLeuLeuCysHisLeuLys	606
2860	Db	2860	-----ATTTRCTT	2868
607	Qy	607	TyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuProArgSerIleGlyLysLeu	626
2869	Db	2869	-----AYATAASVRAGGTACCARAATCGTSGGTAGTAGTG	2904
627	Qy	627	GlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAlaLeuProSerGluIle	646
2905	Db	2905	AASCACTTGGCGTATCTTAATCTATCWGAACTTAAATCAACATTTTACCAGAAWATKTC	2964
647	Qy	647	SerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPheHisTyrAspAsnPhe	666
2965	Db	2965	TGCAATCTTTATAATTACARACCCGTGATTGKTCTGGCTGTGAMTAT	3012
667	Qy	667	SerLeuAsnHisProMetLysCysIleThrAsnThrIleCysLeuProLysValPheThr	686
3013	Db	3013	-----TTAGTTAAKTTGCCCAACACCTCTCA	3039

Qy 687 ProLeuValSerArgAspArgAlaValGlnLeuHisMetAlaThrIys 706  
Db 3040 AASCTT-----AAAAATTGCASCATTTTGACATGAGGRTACT 3078  
Qy 707 SerCysTrpSerGluSerIleGlyValIysValProIysGlyIleGlyValLeuAsp 726  
Db 3079 CKAAKTTAAR-----AACATGCCCTTARGGATTTGTGARTTGAART 3123  
Qy 727 LeuGlnValLeu---GluTyrValAspIleArgThrSerSerArgAlaIleIysGlu 745  
Db 3124 CTACAAACTCTCTTWMGTAAACATTCGCATAGCAATAACCGAGCTTAAGAAGTGCMAAY 3183  
Qy 746 Leu-----GlyGlnLeuSerIysLeuArgIys---LeuGlyValThr 758  
Db 3184 CTCATGGGAARATTTGTATTCGGCGGCTGGGAAATATGGAATCGMTGKGATGCGACG 3243  
Qy 759 ThrAsnGlySerThrIysGluIysCysIysIleLeuTyrAlaIleGluIysLeuSer 778  
Db 3244 TTAAGCGAACTGTCTCANAAAAAGTTWAATGARTTANAACTGCRWTKGGGGTGATR 3303  
Qy 779 SerLeuGlnSerLeuHisValAspAlaIleGlyIleSerAspGlyIleThrLeuGluCys 798  
Db 3304 AATTTAATG-----TTTTCCGAATGGGAACACTTGAATA 3339  
Qy 799 LeuAspSer----- 801  
Db 3340 ANAAGGTCTCAATGAATGAATGCTCATATGCTATCTCAAWAARRRYVWTARWA 3399  
Qy 802 ----- 804  
Db 3400 TTMGKAWRKGGKTYATRTKTMVRAAWAGRGTKKKARGTAGTGTTCATCCCAAT 3459  
Qy 806 ProPro-LeuLeuArgThrLeuValLeuAspGlyIleLeuGluGluMetProAsnTrp-- 824  
Db 3460 CACCCAGGCGAAATAGATGATATTTTCAGGCGCTACTGATGATG--TGGAG 3513  
Qy 825 -----IleGluGlnLeuThrHisLeuIysIle 834  
Db 3514 AGTATGATAGGTTNTCTGGGCGGTAGAGAAATAAGCATCCATCTTGTGAATGAAT 3573  
Qy 835 ---TyrLeuLeuArgSerIysLeuIysGluGlyIleThrMet-----Le 848  
Db 3574 AAGATATYTGCGAATCAGAGCAGGAGCAAGTAAGTCTTATGATGAATTAAGAAGTT 3633  
Qy 848 uIleLeuGlyAlaLeuProAsnLeuMetValLeu-----HisLe 861  
Db 3634 GGATTTAGTGAATGTGAAATTTGGTGAGTTTAGGGGAGAAAAAGGAGGATAATCAT-- 3691  
Qy 861 uTyrArgAsnAlaTyrLeuGlyGluIysLeu-----ValPheIly 874  
Db 3692 -----AATATTAATAGTGGGAGCAGCCTAACATCTTTTAGGAGGTGTAATGTATGGAG 3744  
Qy 874 sThrGlyAlaPheProAsnLeuArg-----ThrLeuTrpIleTyrGl 888  
Db 3745 ATGTAAACCTTTGGAGCATTCAGGTGTCCAGATAGCATGCGAATTTGTATGACAT 3804  
Qy 888 uLeuAspGlnLeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGluIysI 908  
Db 3805 GTGTGATTCAATNACATCCGCTCTCTCCCAACAGGAGGAGGAGCAGACATCAAGTCACT 3864  
Qy 908 eGluIleGlyGluCysArg-----LeuGluSerGlyIleThrGly----- 921  
Db 3865 TACCATCACTGATTCGAAGAAGCTTTCCGAAGAGGAGGTTCGGAGGAGCAGAGAGCAAG 3924  
Qy 922 ----IleIleHis-----LeuProIysLeuIysGluIleProIleArgTyrGlySerIly 938  
Db 3925 AGTGCTTAATAACTCAAAATGCAGATCTTGAATCAGTAGATATAGTAATTTGGCCAAA 3984  
Qy 938 sValIalaGlyLeuGlyGlnLeuGluGlyGluValAsnAlaHisProAsnArg----- 955  
Db 3985 TCTGAAATCTATCAGTGAATTTGATGCTTCATT-----CACCTGAACAGAGATTATAT 4038

Qy 956 -----ProValLeuLeuMetTy. 961  
Db 4039 ATCAAACTGTCGAGTRTGGAGTCATTTCTGACCATGAGTTGCCAAATCTCACCTCCTT 4098  
Qy 961 rSerAspArgArg 965  
Db 4099 AACAGATCGAAGG 4111

RESULT 15  
US-08-930-996A-1  
; Sequence 1, Application US/08930996A  
; Patent No. 6100449  
; GENERAL INFORMATION:  
; APPLICANT: FLUHR, Robert  
; APPLICANT: ESHED, Yuval  
; APPLICANT: ORI, Naomi  
; APPLICANT: PARAN, Ilan  
; APPLICANT: ZAMIR, Daniel  
; TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE  
; TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND  
; TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/930,996A  
; FILING DATE: 09-DEC-1997  
; PRIOR APPLICATION DATA: PCT/US96/05272  
; APPLICATION NUMBER: 15-APR-1996  
; FILING DATE: 15-APR-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 113,373  
; FILING DATE: 13-APR-1995  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4946 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 299..3958  
; US-08-930-996A-1

Alignment Scores:  
Pred. No.: 1.85e-54 Length: 4946  
Score: 580.50 Matches: 249  
Percent Similarity: 42.7% Conservative: 185  
Best Local Similarity: 24.5% Mismatches: 377  
Query Match: 11.0% Indels: 207  
DB: 3 Gaps: 44

US-10-656-394A-8 (1-1032) x US-08-930-996A-1 (1-4946)

Qy 3 GluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerIysAlaIaSer 22  
Db 302 GAGATGGGTAGCAATTTGGTGGTTCCTCTCTCCTCAGCTTGTGATGTTGTTGAT 361  
Qy 23 AlaAlaAlaAspGluThrSerLeuLeuGlyValGluIys-----AspIleTrp 39  
Db 362 AGGCTTGTCTCTTAATGTTGATGCTGCTCAACATGTTTCCGAAGCATACAGATGATGTTGAG 421

Qy 40 TyrIleLys-----AspGluLeuLysThrMetGlnAlaPheLeuArgAlaGlu 56  
Db 422 CTCCTTTGAGAACTGGGGGACATTTTGTAGCTTCCAAATTTGTGTCATGTCAGAG 481  
Qy 57 LeuMetLysLysAspGluLeuLysValTrpAlaGluGlnIleArg----- 73  
Db 482 AATAAGAAAGCATCAATTTGTGAGCCAGTGGTTACATAGCTTCAGACTGCTGTG 541  
Qy 74 AspLeuSerTyAspIleGluAspSerLeuAspGluPheLysValHisIleGluSerGln 93  
Db 542 GACGCTGCTGAACTTGCATAGAACCAAGTCAATTAATGAACTTTGAGGCTTAAAGTGA 601  
Qy 94 ThrLeuPheArgGlnLeuValLysLeuArgGluArgHisArgIleAlaIleArg----- 111  
Db 602 ACNAGCAACCAAGTAAAGTCACTC-----AACCTGTGCTTGAGTGATGAT 649  
Qy 112 ---IleHisAsnLeuLysSerArgValGluValSerSerArgHisThrArgTyrSer 130  
Db 650 TTCTTTTAAATAGAAAGAGTGTGAAGACACACTATTAAAAA-----CTGAGG 703  
Qy 131 LeuValLysProIleSerSer---GlyThrGluIleAspMetAspSerTyAlaGluAsp 149  
Db 704 TTGGAAGAACAAATTTGCTGCTTGGCTTAAAGAGCATTATTTTCGACCAACAGAA 763  
Qy 150 IleArgAsnGlnSerAlaArgAsnValAspGluAlaGluLeuValGlyPheSerAspSer 169  
Db 764 ACTAGAACACCTTCAACTTCTTGGTGTGATCTGCTATCTTGGAAAGGAAGATGAA 823  
Qy 170 LysLys-----ArgLeuLeuLeuMetIleAspThrAsnAlaAsnAspGlyPro 185  
Db 824 ATAGAGAAATTTGGTGGCGGTTGTGTCTATG---GATCAAGAGCAAAAT----- 874  
Qy 186 AlaLysValIleCysValValGlyMetGlyLeuGlyLysThrAlaLeuSerArgLys 205  
Db 875 CTGGCTGATGCTTATTTGGGAATGGCGGCTGAGTGAAGCAACACTTGTCAAGCC 934  
Qy 206 IlePheGluSerGluGluAspIleArgLysAsnPheProCysAsnAlaTrpIleThrVal 225  
Db 935 GTTTAC---AATGATGAGAGAGTGCAGAAACATTTTGGTTGACGCTTGGTTGTGT 991  
Qy 226 SerGlnSerPheHisArgIleGluLeuLysAspMetIleArgGlnLeuLeuGlyPro 245  
Db 992 TCTGAGGCATATGATGCTTTCAGAAATACCAAAAGGTTTACTTCAAGAA---ATTGATCA 1048  
Qy 246 SerSerLeu-----AspGlnLeuGlnGluGlnGlyLysValValVal----- 261  
Db 1049 ACTGACTTGAAGGCTGATGACAACTTTAATCAGCTACATCAAGTCAAAATGAGGCTGATGAC 1108  
Qy 262 GlnValHisLeuSerGluTyrLeuIleGluGluLeuLysGluLysArgTyrPheVal 281  
Db 1109 AATCTTAATCAGCTACAGTCAATTTGAAGGAAAGCTGAATGGAAGGTTCTTGT 1168  
Qy 282 ValLeuAspLeuTrp-----IleLeuHisAspTrpAsnTrpIleAsnGluIleAla 299  
Db 1169 GTCTTGTAGCTGTGGAATGATAATTAATCCTGAGTGGATGACTTGAAGAACTCTTTT 1228  
Qy 300 PheProLysAsnAsnLysGlySerArgIleValIleThrThrArgAsnValAspLeu 319  
Db 1229 TTA-----CAAGGGGATATAGAGTAAGTATCTTACGACACGTAAGAGAGTGT 1282  
Qy 320 AlaGluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAsp 339  
Db 1283 GCCTTGATGATGATGAGTGGGCAATC-----TACATGGGAATCTCTGTAGTGAAGAC 1336  
Qy 340 AlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLys 359  
Db 1337 TCT---TGGGCTCTATTCAACGACATTCATTAGACGACCAAGATCCCAAGGNACATCA 1393  
Qy 360 AsnMetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIle 379  
Db 1394 GAATTTGAAGAGGTTGGAAAAACAAATTCAGACAAAGTGCAAAGGGTTGCTTTAGCTCTA 1453  
Qy 380 LeuThrIleGlyAlaValLeuAlaThrLys---GlnValSerGluTrpGluLysPheTyr 398

Db 1454 AAAGCAGCTTGTGTGTATGTTACGCGCAATACAGAGTGGTGGGAAACATT----- 1510  
Qy 399 GluHisLeuProSerGluLeu---GluIleAsnProSerLeuGluAlaLeuArgMet 417  
Db 1511 -----TTACGAGTGAATAATATGGAGCTTCCAAGTTGTTGCAATGCTATATACCAAG 1564  
Qy 418 ValThrLeuGlyTyrAsnHisLeuProSerHisIleLysProCysPheLeuTyrLeuSer 437  
Db 1565 CTAATGTTGAGCTCAATGATCTCCCTGCACATTTAAAGCAATGTTGGCTTATGTGCA 1624  
Qy 438 IlePheProGluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGlu 457  
Db 1625 ATATATCCAAAGATTAATCAATTTCCGAAAGACAGCAAGTTATTCCCTGTGGATGCTAAT 1684  
Qy 458 GlyPheValArgProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsn 477  
Db 1685 GGTCTTGTACAT-----CAGTTTCATTCGGGTAAACCAATACITTTATC 1726  
Qy 478 GluLeuIleAsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLys 497  
Db 1727 GAGTTGAGATCAAGATCATTTGTCGAAATGCCTCAGAGCCTTCTGAAAAGAGACGTAGAG 1786  
Qy 498 ThrCysArgIleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGluAsn 517  
Db 1787 GAATTTCTTAATGTCATGACCTTGTCAATGATTTG---GCACAAATGCATCTTCAATCAT 1843  
Qy 518 PheValLeuLeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIle 537  
Db 1844 TGTATAAGTTTGAAGATACAAAGGATCGCATATGTTG---GAACAATGTGGCAC--- 1897  
Qy 538 AlaPheHisGlySerMetSerCysLysThrGlyLeuAspTrpSerIleIleArgSerLeu 557  
Db 1898 -----ATGTCTTATTCAATAGGACAAAGTGGTGAGTTGAGAAATGAAA 1942  
Qy 558 AlaIlePheGlyAspArg----- 563  
Db 1943 TCACCTTTTAATCAGAGCAGCTCAGGACATTACTTCCAATCGATATCCAGTTCCATTAC 2002  
Qy 564 -----ProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeu 579  
Db 2003 TCAAAAAAACTAAGCAAGAGGTTGTCATTAACATACTGCTC---ACACTAAGATCCTTTG 2059  
Qy 580 ArgValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAsp---PheAspArg 598  
Db 2060 AGGCGCACTATCATTTGCTCTCATTACCATGAGTGTGCCAAATGACTTGTATTACAA 2119  
Qy 599 IleAlaLeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSerSerIleTyrSer 618  
Db 2120 TTAAGAGCTC-----CTCAGATTTTGGACCTTTCT---GAGACATCGATTACAAAG 2167  
Qy 619 LeuProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSer---Thr 637  
Db 2168 TTGCGCGGATTCATTTTGTGTGTATTAATCTTAGACACACTTCTCTGTCATCTGTGAA 2227  
Qy 638 TyrIleAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCys 657  
Db 2228 TATCTTGAGGAGTACCGCTGCAGATGGAGAGTTG----- 2263  
Qy 658 IleGlyGlnPheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsn 677  
Db 2264 ATTAACTTGGCTCATCTTTGAC-----ATAGCAAC 2293  
Qy 678 ThrIleCysLeuProLysValPheThrProLeuValSerArgAspAspArgAlaLysGln 697  
Db 2294 ACT-----CGGCGCTTGAAG 2308  
Qy 698 IleAlaGluLeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLys--- 716  
Db 2309 ATC-----CCACTACATCTGAGCAGGTTGAAAGGCTCCAGTGTGTGGGAGCCAGTTT 2365  
Qy 717 -----ValProLysGlyIleGlyLysLeu 724

```
Db 2366 CTTGTAGTGGTGGAGATGGAATATTGGGTGAAGCACCACCACTTATATGATCTCTA 2425
Qy 725 ArgAspLeuGlnValLeuGluTyrValAspIleArgThrSerArgAlaIleLys 744
Db 2426 TCAATTCCTAGAGTGGAAATCTGTTGATAGAGGAGAGCTGTGAAGGCAAGATGAGG 2485
Qy 745 GluLeuGly-GlnLeuSerLysLeuArgLysLeuGly-----ValThrThrAs 760
Db 2486 GAGAAGAATCATGTTGAGCAATTATCATTTGGAGTGGAGTGAAGCATTAGTCTGACAA 2545
Qy 760 nGlySerThrLysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLe 780
Db 2546 TCACAAACAGAAAGAGACATCTTCATGAGCTAGCCACATTAACATTAAGCAGTT 2605
Qy 780 uGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLeuAs 800
Db 2606 GAAATCACTGGATATAGAGGGA----- 2627
Qy 800 pSerIleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGluG1 820
Db 2628 -----CAAAC 2632
Qy 820 uMetProAsnTrpIleGluGlnLeuThrHisLeuLysIleTyrLeuLeuArgSerLys 840
Db 2633 -TTTCCAAACTGGGTAGCTGATCTTTGTTTGAAGCTGGTGCATTTCATCTTAGAAA 2691
Qy 840 sLeuLysGluGlyLysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetValLeuHi 860
Db 2692 CTGCAAGGACTGTTACTCTTCCAGCAGCTAGGCACTCCCTGTTGGAAATTCCTTTC 2751
Qy 860 sLeuTyrArgAsnAlaTyrLeuGlyGluLysLeuValPheLysThrGlyAlaPheProAs 880
Db 2752 CATTAG-AGGGATGCATGG-----GATAGAGTGGT-----GA 2783
Qy 880 nLeuArgThrLeuTTrpIleTyrGluLeu-----AspGlnLeuArgGluIleA 896
Db 2784 CAGAGAGTTCATGGCAGATTGCTCCAAAAGCCTTTAACTCTCTTGTGAAGCTTA 2843
Qy 896 rgPheGluAsp-----GlySerSerProL 904
Db 2844 GATTTGAGATATGCTGAAATGGAAGCAATGGCACACACTAGGAATTGGAGAGTTCCCTA 2903
Qy 904 euLeuGluLysIleGluIleGlyGluCysArgLeuGluSerGlyIleThrGlyIleIleH 924
Db 2904 CACTTGAGAAACTTTCCATTAAATTC----- 2932
Qy 924 isLeuProLysLeuLys---GluIleProIleArgTyrGlySer 937
Db 2933 -----CCTGAGCTCAGTTTGGAGATACCCATCCAATTTTCAAGT 2971
```

Search completed: March 9, 2006, 22:52:14  
Job time : 607 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 9, 2006, 22:42:35 ; Search time 1638 Seconds  
(without alignments)  
5210.011 Million cell updates/sec

Title: US-10-656-394A-8

Perfect score: 5268

Sequence: 1 MAETVLSNARSLVGSALSKA.....SQVITLTNDSEIQTGAQAG 1032

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp  
-Q=/abes/ABSSWEB.spool/US10656394/runat\_09032006\_094024\_748/app.query.fasta\_1  
-DB=Published Applications NA Main -QFMT=fastap -SUFFIX=p2n.rnpbm  
-MINMATCH=0.1 -LOOFCLO=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1  
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct  
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NOR=ext  
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p  
-USER=US10656394 @CEN 1 1 1549 @runat\_09032006\_094024\_748 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA Main:

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	ID	Description
1	5268	100.0	3099	8 US-10-656-394A-7
2	5039	95.7	9090	8 US-10-656-394A-13
3	4942.5	93.8	3276	6 US-10-352-179-92
4	4925	93.5	3096	6 US-10-352-179-88
5	4906	93.1	3099	8 US-10-656-394A-3
6	4906	93.1	3674	8 US-10-656-394A-16
7	4753	90.2	76272	6 US-10-352-179-83
8	4753	90.2	76272	6 US-10-352-179-83

8	4397.5	83.5	4596	7	US-10-437-963-37316	Sequence 37316, A
9	4241.5	80.5	2997	8	US-10-656-394A-11	Sequence 11, Appl
10	3664.5	69.6	2982	7	US-10-437-963-2483	Sequence 2483, Ap
11	3205.5	60.8	3220	6	US-10-352-179-90	Sequence 90, Appl
12	3136	59.5	4147	8	US-10-656-394A-5	Sequence 5, Appl
13	3072	58.2	2982	8	US-10-656-394A-1	Sequence 1, Appl
14	3068.5	58.2	2925	7	US-10-437-963-41016	Sequence 41016, A
15	3063.5	58.2	2940	6	US-10-352-179-84	Sequence 84, Appl
16	2814	53.4	2711	7	US-10-437-963-38603	Sequence 38603, A
17	2762	52.4	2422	8	US-10-656-394A-15	Sequence 15, Appl
18	2575	48.9	2982	6	US-10-352-179-86	Sequence 86, Appl
19	2539	48.2	3024	7	US-10-437-963-7778	Sequence 7778, Ap
20	2484.5	47.2	3492	7	US-10-437-963-49433	Sequence 49433, A
21	1902	36.1	2781	7	US-10-437-963-69440	Sequence 69440, A
22	1878.5	35.7	2439	7	US-10-437-963-74853	Sequence 74853, A
23	1722.5	32.7	2351	6	US-10-352-179-97	Sequence 97, Appl
24	1493	28.3	2265	6	US-10-352-179-96	Sequence 96, Appl
25	1384	26.3	1355	6	US-10-437-963-94753	Sequence 94, Appl
26	1238.5	23.5	2937	7	US-10-437-963-64619	Sequence 64619, A
27	1224	23.2	2967	7	US-10-437-963-54125	Sequence 54125, A
28	1211	23.0	4288	7	US-10-437-963-47020	Sequence 47020, A
29	1210	23.0	2946	7	US-10-437-963-32604	Sequence 32604, A
30	1209.5	23.0	4026	7	US-10-437-963-76118	Sequence 76118, A
31	1209	22.9	2928	7	US-10-437-963-55316	Sequence 55316, A
32	1187.5	22.5	4542	7	US-10-437-963-31644	Sequence 31644, A
33	1135	21.5	3455	7	US-10-437-963-88509	Sequence 88509, A
34	1101	20.9	3618	7	US-10-437-963-32912	Sequence 32912, A
35	1085.5	20.6	2325	7	US-10-437-963-88300	Sequence 88300, A
36	1078	20.5	2799	7	US-10-437-963-12196	Sequence 12196, A
37	1077.5	20.5	2844	7	US-10-354-453-35	Sequence 35, Appl
38	1062.5	20.2	2862	3	US-10-267-718-35	Sequence 35, Appl
39	1062.5	20.2	2862	3	US-10-267-718-35	Sequence 35, Appl
40	1048	19.9	3495	7	US-10-437-963-67624	Sequence 67624, A
41	1034.5	19.6	2954	3	US-09-354-453-34	Sequence 34, Appl
42	1034.5	19.6	2954	3	US-10-267-718-34	Sequence 34, Appl
43	1034.5	19.6	6760	3	US-09-354-453-33	Sequence 33, Appl
44	1034.5	19.6	6760	3	US-10-267-718-33	Sequence 33, Appl
45	1025	19.5	2631	7	US-10-437-963-67623	Sequence 67623, A

#### ALIGNMENTS

RESULT 1  
US-10-656-394A-7  
Sequence 7, Application US/10656394A  
Publication No. US20040210957A1  
GENERAL INFORMATION:  
APPLICANT: Wang et al.  
TITLE OF INVENTION: Cloning and Characterization of the  
FILE OF INVENTION: broad-spectrum resistance gene p12  
FILE REFERENCE: 035718/252062  
CURRENT APPLICATION NUMBER: US/10/656,394A  
CURRENT FILING DATE: 2003-09-05  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 3099  
TYPE: DNA  
ORGANISM: Oryza minuta  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(3099)  
US-10-656-394A-7

Alignment Scores:  
Pred. No.: 0  
Score: 5268.00  
Percent Similarity: 100.0%  
Best Local Similarity: 100.0%  
Query Match: 100.0%  
DB: 8  
Length: 3099  
Matches: 1032  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

US-10-656-394A-8 (1-1032) x US-10-656-394A-7 (1-3099)



Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerIysAla 20  
Db 1 ATGCGGAGAGCGTGTGAGCATGGCGAGGTGGTGGCGAGCGCATCAGCAGGCC 60  
Qy 21 AlaSerAlaAlaAspGluThrSerLeuLeuGlyValGluIysAspIleTrpTyr 40  
Db 61 GCTCCGCTGCTGCGAGCGAGCCAGCCCTCTGCTGGCGGTGAGAAAGACATCTGGTAT 120  
Qy 41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetIysIys 60  
Db 121 ATCAAAGATGAGCTAAACACGATGCAAGCATCTCTAGAGCTGCTGAATATGAAAAAG 180  
Qy 61 LysAspGluLeuLysValTrpAlaGluGlnIleArgAspLeuSerTrpAspIleGlu 80  
Db 181 AAGATGAATATTAAGGTTTGGGAGAGCAATATGCTGACCTGCTCATATGACATGAA 240  
Qy 81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100  
Db 241 GATTCCCTTGTAGTAAATTAAGGTCCATATTGAAAGCCAAACCCCTATTTCGTGAGTTGGTG 300  
Qy 101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisIleLeuLysSerArgValGlu 120  
Db 301 AACTCAGAGACGCCACCGAATGCTATCCGTATCCACAACTTAAATCAAGAGTTGAA 360  
Qy 121 GluValSerSerArgAsnThrArgTyrSerLeuValLysProIleSerSerGlyThrGlu 140  
Db 361 GAAGTGTAGTACGAGAACACACGCTACAGTTTGTAGTCAAGCTTATTTCTCTGCGACAGAG 420  
Qy 141 IleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAspGlu 160  
Db 421 ATTGACATGGATTCCTATGCGAAGACATTCGTATCAGTCAGCTCGCAATGTGGATGAG 480  
Qy 161 AlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThrAsn 180  
Db 481 GCTGAGCTGTGTGGGTTTCTGACTCCAAGAAAAGGCTGCTGAAATGATGATACCAAT 540  
Qy 181 AlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLysThr 200  
Db 541 GCTAATGATGGTCCGGCCAGGTAAATCTGTGTGTGGGATGGGTGTTTAGCAAGACA 600  
Qy 201 AlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsn 220  
Db 601 GCTCTTTTCGAGGAAGATCTTTGAAAGCGAGAGACATAGGAAGAACTTCCCTTGCAAT 660  
Qy 221 AlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArg 240  
Db 661 GCTTGGATTTACAGTGTCAATCAATTTACAGGATGAGCTACTTAAAGATATGATACGC 720  
Qy 241 GlnLeuLeuGlyProSerSerLeuAspGlnLeuGlnGluLeuGlnGlyLysValVal 260  
Db 721 CAACTTCTTGGCCCCAGTTCTCTGGATCACTCTTGCAGAAATTCAGGAGAGTGGTG 780  
Qy 261 ValGlnValHisIleLysSerGluTyrIleuIleGluLeuLysGlyLysArgTyrPhe 280  
Db 781 GTGCAAGTACATCATCTTCTGAGTACTGTATGAGAGAGCTCAAGGAGAAGAGTACTTT 840  
Qy 281 ValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAlaPhe 300  
Db 841 GTTGTCTTAGATGATCATGATTTTACATGATGGAAATGGAAATGAAATTCATTT 900  
Qy 301 ProLysAsnAsnLysGlySerArgIleValIleThrThrArgAsnValAspLeuAla 320  
Db 901 CCTAAGAACATTAAGAGGGGAGTCGAATAGTATTAACCACTCGGAATGTGATCTGCG 960  
Qy 321 GluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAspAla 340  
Db 961 GAGAGGTGTGACACAGCTCATCTGGTGTACCACTTGTATTTCTTGACAGATGACAGTCC 1020  
Qy 341 IleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsn 360  
Db 1021 ATAACTTGTCTAGAGAAAAACAAATATAAATCATGAAGACATGGAATCAAATAAAT 1080

Qy 361 MetGlnLysMetValGluAArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeu 380  
Db 1081 ATGCAAAAGATGGTGTGAACGAATTTGAAATAAATGTGGTGGTCTACCACTTAGCAATCTT 1140  
Qy 381 ThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyrGluHis 400  
Db 1141 ACNATGAGAGTGTGCTTGGCACTAAACAGGTGTCAAGATGGGAGAAATTTCTATGACAC 1200  
Qy 401 LeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgArgMetValThrLeu 420  
Db 1201 CTTCTCTCAGAACTAGAAATAAAACCAAGCCTGGAAGCTTTTGGAGAGAATGGTGACCTA 1260  
Qy 421 GlyTyrAsnHisIleuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePhePro 440  
Db 1261 GGTATACACACCTACCTCCATCCATTTTGAACCATGCTTTTGTATCTAAGATATCTTTCT 1320  
Qy 441 GluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheVal 460  
Db 1321 GAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGATGATAGCAGAAAGGTTTCTT 1380  
Qy 461 ArgProLysValGlyMetThrThrLysAspValGlyLysSerTyrPheAsnGluLeuIle 480  
Db 1381 AGACCAAGGTTGGGATGAGCTAAGGATGTCGGAAGAAAGTACTTTTAATGAGCTAATC 1440  
Qy 481 AsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArg 500  
Db 1441 AACCGAAGTATGATTCAACGATCAAGAGTGGGATGAGCAGGAGAAATAATTAAAGACTTGTG 1500  
Qy 501 IleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGlnAsnPheValLeu 520  
Db 1501 ATTCAATGATATCATCGGTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTTGTATTA 1560  
Qy 521 LeuProMetGlyAspGlySerAspLeuValGlnGlnAsnThrArgHisIleAlaPheHis 540  
Db 1561 TTACCAATGGGAGATGGCTCTGATTTAGTTTCAAGAAAACACTCGGCACATAGCATTCAT 1620  
Qy 541 GlySerMetSerCysLysThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIlePhe 560  
Db 1621 GGGAGTATGCTCGCAAACTGGATTTGGATGGAGATTTATTCGATCATTTAGCTATATTTT 1680  
Qy 561 GlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArg 580  
Db 1681 GGTGACAGACCAAGAGTCTAGCACATGCACTGTGTCAGATCAATTCAGGATGTTCGG 1740  
Qy 581 ValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAla 600  
Db 1741 GTCCTGGATCTTGAAGATGTGACATTTTAATCACTCAAAAAGATTTCCGACCGTATTGCA 1800  
Qy 601 LeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuPro 620  
Db 1801 TTGTTGTGCCACTTGAATATCTTGGATTTGGATTTGGTATCATCATATATTCATCTCC 1860  
Qy 621 ArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAla 640  
Db 1861 AGATCCATTTGGTAAACTTACAGGGCTTACAACTTTGAAACATGCCCGAGCACATACATGCA 1920  
Qy 641 AlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGln 660  
Db 1921 GCATCAACAGTGGATCAGTAACTCCAACTCTCTGCTGCTGATCTCTCGTTATAGGACAG 1980  
Qy 661 PheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCys 680  
Db 1981 TTTCAATATGACAACTTTATGCTAAACCAACCACTTAAAGTGAATGCAATAACACAAATATGC 2040  
Qy 681 LeuProLysValPheThrProLeuValSerArgAspAspArgAlaLysGlnIleAlaGlu 700  
Db 2041 CTGCTTAAAGTATTCACACTTTTAGTGTGCGGATGATCGTGCAAAACAAATTTGCTGAA 2100  
Qy 701 LeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLysGly 720  
Db 2101 TTGCATGCGCCCAACAAAGTTGCTGGTCTGAATCAATCGGTGTGAAGAGTACCACAAAGGA 2160  
Qy 721 IleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgArgThrSer 740

```
|||||
2161 ATAGTAAGTTGCGAGACTTCAGGTTCTAGAGTATGATATCAGCGCGACCACTAGT 2220
QY
741 ArgAlaIleLysGluLeuGlnLeuSerLysLeuArgLysLeuGlyValThrAsn 760
Db
2221 AGGCAATCAAGAGCTGGGCGAGTTAAGCACTGAGGAAATAGGTGTGACACAAAC 2280
QY
761 GlySerThrLysGluLysCysGlyLeuLeuTyAlaAlaIleGluLysLeuSerLeu 780
Db
2281 GGGTCGACAAAGGAAAAATTAAGATATCTTTATGCGACCAATTGAGAAGCTCTTCCCTC 2340
QY
781 GlnSerLeuHisValAlaAlaGlyLysLeuSerAspGlyGlyThrLeuGluCysLeuAsp 800
Db
2341 CAATCTCTCCATGTGGATGCTGCGAGAACTCTCAGATGGTGGACACTTGAGTGCTAGAT 2400
QY
801 SerIleSerProProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGlu 820
Db
2401 TCTATTTCATCTCTCCCTCCCTACTGAGGACACTCGTGTGTGGATGGAATCTTGGAGG 2460
QY
821 MetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIleTyLeuLeuArgSerLys 840
Db
2461 ATGCTTAACGTGATTTGACACCTCACTCACTGAGAGAGATCTACTTATTTAGAGGAAA 2520
QY
841 LeuLysGluGlyThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetValLeuHis 860
Db
2521 CTAAAGGAAGGTAAACCATGCTGATCTTGGGCGACTGCGCCCAACCTCATGTCTTCAT 2580
QY
861 LeuTyArgAsnAlaTyLeuGlyGluLysLeuValPheLysThrGlyAlaPheProAsn 880
Db
2581 CTTTATCGGAATGCTTACTCTTGGGGAAGCTAGTATTTCAAAACAGAGCATTTCCCAAT 2640
QY
881 LeuArgThrLeuTrpIleTyLeuLeuAspGlnLeuArgGluIleArgPheGluAspGly 900
Db
2641 CTTAGACACTTTGATTTATGAATTTGATCAGCTAAGAGAGATCAGATTTGAGCAGCGC 2700
QY
901 SerSerProLeuLeuGluLysIleGluIleGlyCysArgLeuGluSerGlyIleThr 920
Db
2701 AGCTCACCCCTCTTGGAAAGATAGAAATAGGCGAGTGCAGGTGGAAATCTGGGATTA 2760
QY
921 GlyIleIleHisLeuProLysLeuLysGluIleProIleArgTyGlySerLysValAla 940
Db
2761 GGTATCAATTCACCTTCCAAAGCTCAAGGAGATTTCCATTAATAGATACGGAAGTAAAGT 2820
QY
941 GlyLeuGlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeuMet 960
Db
2821 GGGCTTTGGTCACTGGAGGAGAAAGTGAACGACACCAATCGCCCGGTGCTGTCTAATG 2880
QY
961 TyrSerAspArgTyHisAspLeuGlyAlaGluAlaGluGlySerIleGluVal 980
Db
2881 TACAGTGACCGAAGGTATACGACTGGGGCTGAGCGGAGGATCTCTATAGAGTG 2940
QY
981 GlnThrAlaAspProValProAspAlaGluGlySerValThrValAlaValGluAlaThr 1000
Db
2941 CAAACAGCAGATCTCTTCTGATCGCGAAGGATCAGTCACTGATGAGTGAAGCAAGC 3000
QY
1001 AspProLeuProGluGlnGlyGluSerSerGlnSerGlnValIleThrLeuThrThr 1020
Db
3001 GATCCCTTCCGAGCAGGAGGAGAGAGCTCGCAGTTCGAGTGATCAGTTGACGAGC 3060
QY
1021 AsnAspSerGluGluIleGlyThrAlaGlnAlaGly 1032
Db
3061 AATGATAGGAAGAGATAGGCACAGCTCAAGCTGGC 3096
```

## RESULT 2

```
US-10-656-394A-13
; Sequence 13, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE OF INVENTION: broad-spectrum resistance gene P12
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656,394A
```

```
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 99090
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 23216
; OTHER INFORMATION: n = A,T,C or G
US-10-656-394A-13

Alignment Scores:
Pred. No.: 0 Length: 99090
Score: 5039.00 Matches: 983
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 95.7% Indels: 0
DB: 8 Gaps: 0

US-10-656-394A-8 (1-1032) x US-10-656-394A-13 (1-99090)
```

```
QY 40 TyrIleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLys 59
Db 77635 TATATCAAGATGAGCTAAACACGATGCAAGCATTCCTTAGAGCTGCTGAACCTTATGAAA 77694
QY 60 LysLysAspGluLeuLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyAspIle 79
Db 77695 AAGAAAGATGAACTATTAAAGGTTTGGCAGAGCAAAATACGTGACCTGCATATGACATT 77754
QY 80 GluAspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeu 99
Db 77755 GAAGATTCCCTTGATGAATTTAAGGTCATATTGAAGCAACCAACCTATTTCGTGAGTTG 77814
QY 100 ValLysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgVal 119
Db 77815 GTGAAGACTCAGAAAGACCCACCCGANTTGTATCCGTATCCACACCTTAATCAAGAGTT 77874
QY 120 GluGluValSerSerArgAsnThrArgTySerLeuValLysProIleSerSerGlyThr 139
Db 77875 GAAGAAAGTGTAGTAGCAGAAACACACGCTACAGTTTAGTCAAGCCTATTTCCTCTCGCACA 77934
QY 140 GluIleAspMetAspSerTyAlaGluAspIleArgAsnGlnSerAlaArgAsnValAsp 159
Db 77935 GAGATTGACATGGATTCTCTATGCAAGAGACATTCTGTAATCAGTCAGCTCGCAATGTGAT 77994
QY 160 GluAlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThr 179
Db 77995 GAAGCTGAGCTTGTGGGTTTCTGACTCCAGAAAAGGCTGCTTGAATATGATCGATACC 78054
QY 180 AsnAlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLys 199
Db 78055 AATGCTAATGATGTCCGCGCAAGGTAATCTGTGTGTGGATGGGTGGTGTAGGCAAG 78114
QY 200 ThrAlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCys 219
Db 78115 ACAGCTCTTTTCGAGAAAGATCTTTGAAGCGAAGAGACATTAGGAAGAACTTCCCTTGC 78174
QY 220 AsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLysAspMetIle 239
Db 78175 AATGCTTGGATTACAGTGTCAATCATNTTTCACAGGATTTGAGCTACTTAAAGATATGATA 78234
QY 240 ArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuGlnGluLeuGlnGlyLysVal 259
Db 78235 CGCCCAACTTCTTGGCCCCAGTTCTCTGGATCAACTCTTGAAGCAATTTGCAAGGAAGGTG 78294
QY 260 ValValGlnValHisLysLeuSerGluTyLeuIleGluLeuLysGluLysArgTy 279
Db 78295 GTGGTGAAGTACATCATCTTTCTGAGTACTGATAGAAGCTCAAGAGAAAGAGGTAC 78354
QY 280 PheValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAla 299
```

Db 78355 TTTGTTGTTCTAGATGATCTATGGATTTTACATGATTTGGAAATTTGGATAAATGAATTCGA 78414  
Qy 300 PheProLysAsnAsnLysGlySerArgIleValIleThrThrArgAsnValAspLeu 319  
Db 78415 TTTCTTAAAGAAACAATAAGAGGCGAGTCTGAATAGTAATAACCACTCGGAATGTCATCTT 78474  
Qy 320 AlaGluLysCysAlaThrAlaSerLeuValTyRhiLeuAspPheLeuGlnMetAsnAsp 339  
Db 78475 GCGAGAGTGTGCGACAGCTCTACTGGTGATCCCTTGATTTCTTGAGATGAACGAT 78534  
Qy 340 AlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLys 359  
Db 78535 GCCATAAATCTGCTACTGAGAAAAACAATAAATAAANTCATGACATGGAATCAATAAA 78594  
Qy 360 AsnMetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIle 379  
Db 78595 AATATGCCAAAAGATGGTTGAACGAATTTGTAATAAATGTTGGTCTGTACCTATGCAATA 78654  
Qy 380 LeuThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyRglu 399  
Db 78655 CTTACAAATAGGAGCTGTGCTGCAACTAAACAGGTGTGAGATGGGAGAAATCTATGAA 78714  
Qy 400 HisLeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgMetValThr 419  
Db 78715 CACTTCTCTTCAAACTAGAAATAAACCAGCTGGAACCTTTGAGGAAATGGTGACC 78774  
Qy 420 LeuGlyTyRAsnHisLeuProSerHisLeuLysProCysPheLeuTyRLeuSerIlePhe 439  
Db 78775 CTAGGTTACAACCACTACCATCCATTTGAAACCATGCTTTTGTATCTAAGTATCTTT 78834  
Qy 440 ProGluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPhe 459  
Db 78835 CTTGAGGATTTTGAATAAATAAGGAATCGTCTAGTAGTAGATGGATAGCAGAGGGTTT 78894  
Qy 460 ValArgProLysValGlyMetThrThrLysAspValGlyLysSerTyRAsnGluLeu 479  
Db 78895 GTTAGACCAAAAGTTGGATGACGACTAAGGATGTCGAGAAAGTTTACTTTAATGAGCTA 78954  
Qy 480 IleAsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCys 499  
Db 78955 ATCAACCGAAGTATGATTTCAACGATCAAGAGTGGGATGAGGCAAGAAATAAAGACTGT 79014  
Qy 500 ArgIleHisAspIleArgAspIleThrValSerIleSerArgGlnGluAsnPheVal 519  
Db 79015 CGAATTCATGATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAATTTGTA 79074  
Qy 520 LeuLeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPhe 539  
Db 79075 TTATTACCAATGGGAGATGGCTCTGATTTAGTTTACGAGAAACACTCGCCACATGATTC 79134  
Qy 540 HisGlySerMetSerCysLysThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIle 559  
Db 79135 CATGGAGTATGTCCTGCAAAATCGAATTTGGATTTGGGATGATTTATTCATCATGATATT 79194  
Qy 560 PheGlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeu 579  
Db 79195 TTTGGTGACAGACCAAGAGCTAGCACATGCGAGTTTGTCCAGATCAATTTGAGGATGTA 79254  
Qy 580 ArgValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIle 599  
Db 79255 CGGGCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACCGTATT 79314  
Qy 600 AlaLeuLysCysHisLeuLysTyRLeuSerIleGlyTyRSerSerSerIleTyRLeu 619  
Db 79315 GCAATGTTGTGCCACTTGAAATCTTGAATTTGGATTTGGATTTCTGTCATATATTTACCTT 79374  
Qy 620 ProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyRile 639  
Db 79375 CCCAGATCCATTTGTAATACAGGGCTTACAACTTTGAACTGCGGAGCACATACATT 79434  
Qy 640 AlaAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGly 659  
Db 79435 GCAGCACTACCAAGTGAGATCAGTAAACTCCAATGTCTGCTACTCTTCTGTTGTATAGGA 79494

Qy 660 GlnPheHisTyRAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIle 679  
Db 79495 CAGTTTCAATATATGACAACTTTAGTCTAAACCCCAATGAAGTGCATAAACAATA 79554  
Qy 680 CysLeuProLysValPheThrProLeuValSerArgAspAspArgAlaLysGlnIleAla 699  
Db 79555 TGCCTGCCCTAAAGTATTACACCTTTAGTTAGTTCGCGATGATCGTGCAGAAACAAATTCCT 79614  
Qy 700 GluLeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLys 719  
Db 79615 GAAATTCACATGCGCCACCAAAAGTTGCTGCTCTGAATCAATCGGTGTGAAGGTACCCAAA 79674  
Qy 720 GlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyRValAspIleArgThrSer 739  
Db 79675 GGAATAGTAGTATGTCGAGACTTTCGAGGTCTTAGAGTATGATAGTATCAGGCGHACCAT 79734  
Qy 740 SerArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrThr 759  
Db 79735 AGTAGAGCAATCAAAAGAGCTGGCGGCAAGTAAAGCAAGCTGAGGAAATTAGGTGTGACAACA 79794  
Qy 760 AsnGlySerThrLysGluLysCysLysIleLeuTyRAlaAlaIleGluLysLeuSerSer 779  
Db 79795 AACGGTGCAGAAAGGAAATGTAAGATACCTTTATGACGCCATTTGAGAGCTCTCTTCC 79854  
Qy 780 LeuGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLeu 799  
Db 79855 CTCCAAATCTCTCCATGATGATGCTGCGAGGAATCTCAGATGTTGGAACACTTGTAGTGCCTA 79914  
Qy 800 AspSerIleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGlu 819  
Db 79915 GATCTATTTCT 79974  
Qy 820 GluMetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIleTyRLeuLeuArgSer 839  
Db 79975 GAGATGCTTAACCTGATGAGAGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 80034  
Qy 840 LysLeuLysGluGlyLysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetValLeu 859  
Db 80035 AAATCAAGGAGGATGAAACCATGCTGATGATCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAG 80094  
Qy 860 HisLeuTyRArgAsnAlaTyRLeuGlyLysLeuValPheLysThrGlyAlaPhePro 879  
Db 80095 CATCTTTATCGAATGCTTACCTTTGGGAGAGAGCTAGTATTTCAAAACAGGAGCACTTCCCA 80154  
Qy 880 AsnLeuArgThrLeuTrpIleTyRLeuAspGlnLeuArgGluIleArgPheGluAsp 899  
Db 80155 AATCTTAGAACACTTTGGATTTATGAATTTGATGATGATGATGATGATGATGATGATGATGATG 80214  
Qy 900 GlySerSerProLeuLeuGluLysIleGluIleGlyGlyCysArgLeuGluSerGlyIle 919  
Db 80215 GGCAGCTCACCCCTGTTTGAAGAGATAGAAATAGGCGAGTGCAGGTTTGAATCTGGGATT 80274  
Qy 920 ThrGlyIleIleHisLeuProLysLeuLysGluIleProIleArgTyRLeuSerIleVal 939  
Db 80275 ACTGGTATCATCTCACTTCAAGAGCTCAAGAGGATTTCCAAATTTAGATAGCGAAGTAAAGTG 80334  
Qy 940 AlaGlyLeuGlyGlnLeuGluGlyValAsnAlaHisProAsnArgProValLeuLeu 959  
Db 80335 GCTGGGCTTGGTTCAGCTGGAGGAGAGTGAACGACACACCCCAATCGCCCGTCTGCTA 80394  
Qy 960 MetTyRSerAspArgArgTyRHisAspLeuGlyAlaGluAlaGluGlySerSerIleGlu 979  
Db 80395 ATGTACAGTACCGAAGGATCACGACTGGGGGCTGAAGCGAAGGATCTCTTATAGAA 80454  
Qy 980 ValGlnThrAlaAspProValProAspAlaGluGlySerValThrValAlaValGluAla 999  
Db 80455 GTGCAAAACAGCAGATCTCTGTTCTGATGCGAAGGATCAGTCTGATGATGATGATGATGATGAT 80514  
Qy 1000 ThrAspProLeuProGluGlnGlyLysSerGlnSerGlnSerGlnValIleThrLeuThr 1019  
Db 80515 ACGGATCCCCCTTCCGAGCAGGAGGAGAGAGCTCGCAGTGCAGGATGATCAGCTTTCAGC 80574



Qy 482 ArgSerMetIleClnArgSerArgValGlyIleAlaGlyIleLysIleLysThrCysArgIle 501  
Db 1621 CGAAGTATGATTCACAGATCAAGAGTGGGCATATCAGGAAATAATTAAGACTTGTGCAATC 1680  
Qy 502 HisAspIleIleArgAspIleThrValSerIleSerArgGlnGlnAenPheValLeuLeu 521  
Db 1681 CATGATATCATCGTGATATACAGTTCAATCTCGAGACAGGAAATTTGTATGTTA 1740  
Qy 522 ProMetGlyAspCysSerAspLeuValGlnGlnAenThrArgHisIleAlaPheHisGly 541  
Db 1741 CCAATGGGAGATGGCTCTGATTTAGTTTACAGGAAACATCCGCCACATAGCATTTCCATGGG 1800  
Qy 542 SerMetSerCysIleThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIlePheGly 561  
Db 1801 AGTATGTCCTGCACAAACAGGATTTGGATTGGAGCATTTATCGATCATTTATTTGGT 1860  
Qy 562 AspArgProIleSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArgVal 581  
Db 1861 GRACAGACCCAGAGTCTAGCACATGACATGCTTTGTCTAGATCAATTTGAGGATGTTTACGGGTC 1920  
Qy 582 LeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAlaLeu 601  
Db 1921 TTGGATCTTGAAGATGTGACATTTCTATCATCTCAAAAGATTTGACCGGATTTGCAATG 1980  
Qy 602 LeuCysHisLeuLysIleSerIleGlyIleThrSerSerIleIleArgSerLeuProArg 621  
Db 1981 TTGTGGCCACTTGAAATACCTTGAATTTGATTTGATTTGATTTGATTTGATTTGATTTG 2040  
Qy 622 SerIleGlyLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrIleAlaAla 641  
Db 2041 TCCATTTGGTAACTACAGGGCTACAACTTTTGAACATGCTGAGAACATACATTCGAGCA 2100  
Qy 642 LeuProSerGluIleSerIleLysLeuGlnCysLeuHisThrLeuArgCysIleGlnPhe 661  
Db 2101 CTACCAAGTCAGATCAGTAAATCTCCAAATGCTGCATATCTCTGCTGTAGTAAAGTTT 2160  
Qy 662 HisTrpAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCysLeu 681  
Db 2161 GTTTATGACACTTTAGTCTAAACCCCAATGAAGTGCAATCTAACCAATATGCTCTG 2220  
Qy 682 ProLysAlaPheThrProLeuValSerArgAspArgAlaLysGlnIleAlaGluLeu 701  
Db 2221 CCTAAAGTATTCACACCTTTAGTTAGTCGATGATCGTCAAAACAAATTTGCTGAATG 2280  
Qy 702 HisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValPheLysGlyIle 721  
Db 2281 CACTGGCCACCAAGTTGCTGCTGATCATTCGCTGAGGTACCCAAAGAAATA 2340  
Qy 722 GlyLysLeuArgAspLeuGlnValLeuGluThrValAspIleArgThrSerArg 741  
Db 2341 GGTAAAGTTGCGAGACTTGCGAGTTCTAGAGTATGATATATAGGCGGACCAAGTAGTA 2400  
Qy 742 AlaIleLysGluLeuGlyGlnLeuSerLysIleLeuArgLysLeuGlyValThrThrAsnGly 761  
Db 2401 GCATCAAGAGCTGGGCACTTAAAGCTTGAAGATTTAGGTGATTAACAAAGGC 2460  
Qy 762 SerThrLysGluLysCysLysIleLeuThrAlaIleGluLysLeuSerSerLeuGln 781  
Db 2461 TCGACAAAGGAAATGTAAGATATCTTTATGACGCCATTCGAGAAGCTCTCTCCCTCCAA 2520  
Qy 782 SerLeuHisValAspAlaAlaGlyLysSerAspCysGlyThrLeuGluCysLeuAspSer 801  
Db 2521 TCTCTATGTGAATGCTGGCTTATTCAGATTTGAAACATTCGAGTGGCTTAGATCT 2580  
Qy 802 IleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGluMet 821  
Db 2581 ATTATCATCTCTCTCCCTACTGAGGACACTCGGGTTGAATGAAAGTCTTCAAGAGATG 2640  
Qy 822 ProAsnTrpIleGluGlnLeuThrHisLeuLysIleLysIleThrLeuArgSerLysLeu 841  
Db 2641 CCTAATGGATTTGAGAGCTCCTACCTGGAAGAATCTTACTTTATGAGGAGCAACTA 2700

Qy 842 LysGluGlyLysThrMetLeuIleLeuGlyAlaIleProAsnLeuMetValLeuHisLeu 861  
Db 2701 AAGGAGGTAAACCATGCTGATACTTTGGGGCATTTGCCAACCTCATGCTCTTTATCTT 2760  
Qy 862 TyrArgAsnAlaLysLeuGlyGluLysLeuValPheLysThrGlyAlaPheProAsnLeu 881  
Db 2761 TATTGGAATGCTTACCTTTGGGAGAACCTAGTATTCAAAACGGGAGCATTTCCCAATCTT 2820  
Qy 882 ArgThrLeuTrpIleThrGluLeuAspGlnLeuArgLysLeuIleArgPheGluAspGlySer 901  
Db 2821 AGAACACATCTCGATTTTACGAATTTGATTCAGTCAAGAGATGATGATTTTGAAGATGGCAGC 2880  
Qy 902 SerProLeuLeuGluLysIleGlyGlyCysArgLeuGluSerGlyIleThrGly 921  
Db 2881 TCACCCCTGTTTGGAAAAGATAGAAATCTCTTGTCTGCGAGTTGGATTCAGGATTTATGCT 2940  
Qy 922 IleIleHisLeuProLysLeuLysGluIleProIleArgTyrCysSerLysValAlaGly 941  
Db 2941 ATCATTTCACTTCCAAAGCTCAAGGAGATTTCACTTGAATACAAAGTAAAGTGGCTAGG 3000  
Qy 942 LeuGlyGlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeuMetTyr 961  
Db 3001 CTTGTCTAGCTGGAGGAGAGTGAACACACACCCCAATCGCCCTGCTGCGAATGGAC 3060  
Qy 962 SerAspArgArgTyrHisAspLeuGlyAlaGluAlaGluGlySerSerIleGluValGln 981  
Db 3061 AGTGACCGAAGGATTCACGACCTGGGGGCTGAAAGCCGAGGATCTTCTATAGAAGTGCAA 3120  
Qy 982 ThrAlaAspProValProAspAlaGluGlySerValThrValAlaValGluAlaThrAsp 1001  
Db 3121 ACAGCAGATCTCTTCTGATGCCAAGGATCAGTCACTGTAGCAGTGGAGCAACGAT 3180  
Qy 1002 ProLeuProGluGlnGluGlyGluSerSerGlnSerGlnValIleThrLeuThrAsn 1021  
Db 3181 CCCCTTCCGAGCAGGAGGAGAGCTGCGAGTCCGAGTGCAGTGCAGTGCAGTGCAGCAGC 3240  
Qy 1022 AspSerGluGluIleGlyThrAlaGlnAlaGly 1032  
Db 3241 GATAGGAGAGATAGGACACAGCTCAAGCTGGC 3273

## RESULT 4

US-10-352-179-88  
; Sequence 88, Application US/10352179  
; Publication No. US20040006789A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Guo-liang  
; APPLICANT: Liu, Guifu  
; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pl.  
; FILE REFERENCE: 22727/04108  
; CURRENT APPLICATION NUMBER: US/10/352,179  
; CURRENT FILING DATE: 2003-01-27  
; PRIOR APPLICATION NUMBER: 60/352,106  
; PRIOR FILING DATE: 2002-01-25  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 88  
; LENGTH: 3096  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(3096)  
; OTHER INFORMATION:  
US-10-352-179-88

Alignment Scores:  
Pred. No.: 0 Length: 3096  
Score: 4925.00 Matches: 976  
Percent Similarity: 96.9% Conservative: 14  
Best Local Similarity: 95.5% Mismatches: 32  
Query Match: 93.5% Indels: 0  
DB: 6 Gaps: 0



US-10-656-394A-8 (1-1032) x US-10-352-179-88 (1-3096)

QY 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20  
Db 1 ATGGCGGAGACGGTCTGAGCATGGCGAGGTCTGCTGGTGGGCACTGCCATCAGCAAGGCC 60  
QY 21 AlaSerAlaAlaAAspGluThrSerLeuLeuGluValGluLysAspIleThrTyr 40  
Db 61 GCCTCTGGCGGTGCCAATAGACAGCGCTCTGCTGGCGGTGGAGAAGGACATCTGGTAT 120  
QY 41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysLys 60  
Db 121 ATCAAGATGAGCTAAACCAATAGCAGCAATCTCTAGAGCTGCTGAGATGATGAAGAAG 180  
QY 61 LysAspGluLeuLysValTTPAlaGluGlnIleArgAspLeuSerTyrAspIleGlu 80  
Db 181 AAAGATGAACATTAAGGTTTGGCAGAGCAATACGTGACCTGCTGATGACATTTGAA 240  
QY 81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100  
Db 241 GATTCCTTGGATGAATTTAAAGTCCATATTGAAGCCAAACCTCTATTCTGTCAGTTGGTG 300  
QY 101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGlu 120  
Db 301 AAACCTTAGAGCGCCACCGGATCGCTATCGGTATCCACCAACCTCAATCAAGAGTTGAA 360  
QY 121 GluValSerSerArgAsnThrArgTyrSerLeuValLysProIleSerSerGlyThrGlu 140  
Db 361 GAAGTGAGTAGAGAGAACACACGCTACAAATTTAGTCGAGCTATTTCTCCCGGCACAGAG 420  
QY 141 IleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAspGlu 160  
Db 421 GATGACATGATTCCTATGTCAGAGACATTCGCAATCAATCAGCTCGAAATGCGATGAA 480  
QY 161 AlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThrAsn 180  
Db 481 GCTGAGCTTGTGGGTGTTCTGACTCCAAAGAAAGGCTGCTTGAATGATCGATACCAAT 540  
QY 181 AlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLysThr 200  
Db 541 GCTAATGATGCTCGGCCACAGGATATCTGCTGTTGGATGGGTGTTAGGCAAGACA 600  
QY 201 AlaLeuSerArgLysIlePheGluSerGluLysPheArgLysAsnPheProCysAsn 220  
Db 601 GCTCTTTTCGAGGAGATCTTTGAAAGCGAAGACATAGGAGAACTTCCCTTCGATT 660  
QY 221 AlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArg 240  
Db 661 GCTTGGATTACAGTGTCAATCATTTTCAAGGATTCAGCTACTTAAAGATATGATACGC 720  
QY 241 GlnLeuLeuGlyProSerSerLeuAspGlnIleuGlnIleuGlnIleLysValVal 260  
Db 721 CAACCTCTTGGGCCCGGATCTCTGGATCAACTCTTGAAGAAATTTGAAGGAAAGGTGGT 780  
QY 261 ValGlnValHisIleLeuSerGluTyrLeuIleGluGluLeuLysGluLysArgTyrPhe 280  
Db 781 GTCAAGTACATCACTTCTGAGTACTCTGATAGAGAGCTCAAGGAGAGAGGTACTTT 840  
QY 281 ValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAlaPhe 300  
Db 841 GTTATTCTAGATGATCTATGGATTTTACATGATTTGGAATTTGGAATTAATTTGCAATTT 900  
QY 301 ProLysAsnAsnLysLysGlySerArgIleValIleThrArgAsnValAspLeuAla 320  
Db 901 CCTAAGAACATTAAGAGGCGAGTGCATATGATATACCCTCGGATGTTGATCTAGCG 960  
QY 321 GluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAspAla 340  
Db 961 GAGAAGGTGCCACAGCCTCACTGGTGTACCACTTGTATTTCTTTCGAGATGAACGATGCC 1020  
QY 341 IleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsn 360  
Db 1021 ATACATTTGCTACTGAGAAAAACAAATAAATATCATGATGATGATGATGATGATGATGAT 1080

QY 361 MetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeu 380  
Db 1081 ATGCAAAGAGATGGTTGAACGAATTTAAATAATGGTGGTCTACCATTTAGCAATACTT 1140  
QY 381 ThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyrGluHis 400  
Db 1141 ACAATAGGAGCTGTGCTTGCACACTAAACATGTGTCAAGATGGAGAAATTTCTATGAACAA 1200  
QY 401 LeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgMetValThrLeu 420  
Db 1201 CTTCTCTCAGAACTAGAAATAAAACCCAGCCTGGAGCTTTGAGGAGAAATGGTGACCTTA 1260  
QY 421 GlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLysSerIlePhePro 440  
Db 1261 GGTATCAACACCTACCATCCCATCTGAAACCATGCTTTTGTATCTAAGATATCTTCT 1320  
QY 441 GluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheVal 460  
Db 1321 GAGGATTTTGAATCAAAAGCAATCGTCTAGTAGGTAGATGGATAGCAGAGGGTTTGT 1380  
QY 461 ArgProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeuIle 480  
Db 1381 AGACCAAGGTTGGATGACACATAGCATGTCCGAGAAAGTTACTTTAATGAGCTAATC 1440  
QY 481 AsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArg 500  
Db 1441 AACCGAAGTATGATCAACGATCAAGAGTGGCATAGCAGGAAAAATTAAGACTTTGCGA 1500  
QY 501 IleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGlnAsnPheValLeu 520  
Db 1501 ATCCATGATATCATCCGCGATATCACAGTTTCAATCTCGAGACAGGAAATTTTGTATTA 1560  
QY 521 LeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHis 540  
Db 1561 TTACCAATGGGAGATGGCTCTGATTTAGTTTCAAGAAAAACATCGCCACATAGCATTCAT 1620  
QY 541 GlySerMetSerCysLysThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIlePhe 560  
Db 1621 GGGATGTATGCTCGCAAAACAGGATTTGGATGGAGCATATTCATCATTTAGCTATTTT 1680  
QY 561 GlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArg 580  
Db 1681 GGTGACAGACCAAGAGTCTAGCACATGTCAGTTTGTCTAGATCAATTTAGGATGTTACGG 1740  
QY 581 ValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAla 600  
Db 1741 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTCCAGCGTATGCA 1800  
QY 601 LeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuPro 620  
Db 1801 TTGTTGTGCCACTTGAATACTTTCAGTATTTGGATATTCGTATTCATCATATTCACCTCC 1860  
QY 621 ArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAla 640  
Db 1861 AGATCCATTTGGTAAACTACAGCGCTTCAAACTTTTGAACATGCTGAGACATACATGCA 1920  
QY 641 AlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGln 660  
Db 1921 GCACCTACCAAGTGAGATCAGTAACTCCAATGTCTGCATCTCTTCTGTTAGTAGAAG 1980  
QY 661 PheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCys 680  
Db 1981 TTTGTTTATGACAACTTTTAGTCTAAACCCCAATGAAGTGCAATACTAACCAATATGC 2040  
QY 681 LeuProLysValPheThrProLeuValSerArgAspAspArgAlaLysGlnIleAlaGlu 700  
Db 2041 CTGCTTAAAGTATTTCACTTTTAGTTAGTGTGCGATGATCGTGCAGAAACAAATTTGCTGAA 2100  
QY 701 LeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLysGly 720  
Db 2101 TTGCACATGGCCACCAAAAGTTGCTGTGATCTGAATCATTTCCGTTGTGAAGGTACCCAAAGGA 2160



```
Qy 721 IleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgThrSerSer 740
Db 2161 ATAGGTAAAGTTCGAGACTTCGAGGTTCAGAGTATGTAGATATCAGCGCGACAGTAGT 2220
Qy 741 ArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrAsn 760
Db 2221 AGAGCAATCAAGAGCTGGGGCACTTAAGCAAGTTGAGGAAATAGGTGTGATAACAAA 2280
Qy 761 GlySerThrLysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLeu 780
Db 2281 GGCTCGCAAGAGAAAGAAAGTAAAGTACTTTATGAGCCATTTGAGAGCTCTCTCCCTC 2340
Qy 781 GlnSerLeuHisValAspAlaAlaGlyLysSerAspGlyGlyThrLeuGluCysLeuAsp 800
Db 2341 CAATCTCTCTATGTAATGCTGCTTTATCAGATATTGAACACATTTAGTGCCTAGAT 2400
Qy 801 SerLeuSerProProLeuLeuArgThrLeuValLeuAspGlyLysLeuGluGlu 820
Db 2401 TCTATTTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
Qy 821 MetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeuArgSerLys 840
Db 2461 ATGCTTAACCTGATGAGCAGCTCACTCACTGAGAGAGATCTACTATTATGAGGAGCAA 2520
Qy 841 LeuLysGluGlyLysThrMetLeuLeuLeuLeuGlyAlaLeuProAsnLeuMetValLeuHis 860
Db 2521 CTAAGAGAGAGTAAACCACTGCTGATCTGAGGAGGAGTATTCACCAAGGAGGAGTAT 2580
Qy 861 LeuTyrArgAsnAlaTyrLeuGlyGluLysLeuValPheLysThrGlyAlaPheProAsn 880
Db 2581 CTTTATGGAATGCTTACCTTGGGAGAGAGTATTCACCAAGGAGGAGTATTCACCAAT 2640
Qy 881 LeuArgThrLeuTrpIleTyrGluLeuAspGlnLeuArgGluLysLeuArgPheGluAspGly 900
Db 2641 CTTAGAACCTTCTGATTTACCAATTTGAGTATGAGTATGAGTATGAGTATGAGTATGAG 2700
Qy 901 SerSerProLeuLeuGlyLysIleGluLysGlyCysArgLeuGluSerGlyLysThr 920
Db 2701 AGCTCACCTCTGTGGAGAGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 2760
Qy 921 GlyLysLeuHisLeuProLysLysLysLysLysLysLysLysLysLysLysLysLys 940
Db 2761 GGATATCATTCACCTTCAAGGCTCAAGGAGATTTTCACTTGAATCAAAAGTAAAGTGGCT 2820
Qy 941 GlyLeuGlyGlnLeuGluGluValAlaAsnAlaHisProAsnArgProValLeuLeuMet 960
Db 2821 AGGCTTGTGCTGAGGAGGAGAGTGAACACACACACACACACACACACACACACACAC 2880
Qy 961 TyrSerAspArgTyrHisAspLeuGlyAlaGluLysSerSerLysLysLysLysLys 980
Db 2881 GACAGTGACCGAAGGAGTCAACGACCTGGGGGCTGAAGCCGAAGGATCTTCTATAGAAGTG 2940
Qy 981 GlnThrAlaAspProValProAspAlaGluGlySerValThrValAlaValGluAlaThr 1000
Db 2941 CAACACGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3000
Qy 1001 AspProLeuProGluGlnGluGlySerSerGlnSerGlnValIleThrLeuThrThr 1020
Db 3001 GATCCCTCTCCGAGGAGGAGGAGAGCTCGAGTGCAGGTGATCACTGAGTGAAGAGG 3060
Qy 1021 AsnAsp 1022
Db 3061 AACGAT 3066
```

## RESULT 5

US-10-656-394A-3

; Sequence 3, Application US/10656394A

; Publication No. US20040210957A1

; GENERAL INFORMATION:

; APPLICANT: Wang et al.

; TITLE OF INVENTION: Cloning and Characterization of the

; TITLE OF INVENTION: broad-spectrum resistance gene P12

; FILE REFERENCE: 035718/252062

```
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3099
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3099)
; US-10-656-394A-3

Alignment Scores:
Pred. No.: 0 Length: 3099
Score: 4906.00 Matches: 971
Percent Similarity: 96.0% Conservative: 20
Best Local Similarity: 94.1% Mismatches: 41
Query Match: 93.1% Indels: 0
DB: 8 Gaps: 0
```

US-10-656-394A-8 (1-1032) x US-10-656-394A-3 (1-3099)

```
Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20
Db 1 ATGGCGGAGACGGTCTGAGCATGGCGAGGTGCTGGTGGGCGAGTGCATCAGCAAGGCC 60
Qy 21 AlaSerAlaAlaAspGluThrSerLeuLeuLeuGlyValGluLysAspIleTyrTyr 40
Db 61 GCCTCTGGCGCTGCCAATGAGACGAGCTCTCTCGCGCTCGAGAAGGACATCTCGTAT 120
Qy 41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysLys 60
Db 121 ATCAAGATGAGCTTAAACCAATCAGGCAATTCCTTAGAGCTGCTGAAGTTATGAAAAAG 180
Qy 61 LysAspGluLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGlu 80
Db 181 AAAGATGAACATTAAAGGTTTGGGAGAGCAATACGTGCCTGCTGATGACATTGAA 240
Qy 81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100
Db 241 GATTCCTTGTAGTAATTTAAAGTCCATATTGAAAGCCAAACCTATTTCGTAGTTGGTG 300
Qy 101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGlu 120
Db 301 AAACCTAGAGAGCGCCACCGGATCGCTATCGTATCCACCACTCAATCAAGAGTTGAA 360
Qy 121 GluValSerSerArgAsnThrArgTyrSerLeuValLysProIleSerSerGlyThrGlu 140
Db 361 GAAGTGAGTAGCAGGAACACACGCTACAAATTTAGTCGAGCCTATTTCTCCGCGCAGAG 420
Qy 141 IleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAspGlu 160
Db 421 GATGATCATGGATTCCTATGAGAGAGACATTCGCATCAATCAGCTCGAATGTGGATGAA 480
Qy 161 AlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThrAsn 180
Db 481 GCTGAGCTTTGGTGGTCTTCTGACTCAAGAAAAGGCTGCTTGAATATGATCGATACCAAT 540
Qy 181 AlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyLysLeuGlyLysThr 200
Db 541 GCTAATGATGCTCCGGCCNAGTAAATCTGTGTGTGGGATGGGTGGTGTGGCAAGACA 600
Qy 201 AlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsn 220
Db 601 GCTCTTTTCGAGGAGATCTTTGAAAGCGAAGAGACATTAGAGGAAGAACTTCCCTTGCAT 660
Qy 221 AlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArg 240
Db 661 GCTTGGATTACAGTGCACATCATTTCAAGAGTTAGGCTACTTAAAGATATGATACGC 720
Qy 241 GlnLeuLeuGlyProSerSerLeuAspGlnLeuLeuGlnLeuGlnLysValVal 260
```



QY 981 GlnThrAlaAappProValProAspAlaGluGlySerValThrValAlaValGluAlaThr 1000  
 Db 2941 CAAACAGCAGATCCCTGTTCCCTGATGCCCAAGAGATCACTGATGAGCAGTGGAGCAACG 3000  
 QY 1001 AspProLeuProGluGlnGluGlyGluSerSerGlnSerGlnValIleThrLeuThrThr 1020  
 Db 3001 GATCCCTTCCGAGCAGGAGAGAGAGCTCGCAGTGCAGGTGATCAGCTTGAAGCAGC 3060  
 QY 1021 AnAspSerGluGluIleGlyThrAlaGlnAlaGly 1032  
 Db 3061 AATGATAGCGAAGAGATAGGACAGCTCAAGCTGGC 3096

RESULT 6

US-10-656-394A-16  
 ; Sequence 16, Application US/10656394A  
 ; Publication No. US20040210957A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang et al.  
 ; TITLE OF INVENTION: Cloning and Characterization of the  
 ; FILE OF INVENTION: broad-spectrum resistance gene p12  
 ; FILE REFERENCE: 035718/252062  
 ; CURRENT APPLICATION NUMBER: US/10/656.394A  
 ; CURRENT FILING DATE: 2003-09-05  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: FastSeq For Windows Version 4.0  
 ; SEQ ID NO 16  
 ; LENGTH: 3674  
 ; TYPE: DNA  
 ; ORGANISM: Oryza minuta  
 US-10-656-394A-16

Alignment Scores:  
 Pred. No.: 0 Length: 3674  
 Score: 4906.00 Matches: 971  
 Percent Similarity: 96.0% Conservative: 20  
 Best Local Similarity: 94.1% Mismatches: 41  
 Query Match: 93.1% Indels: 0  
 DB: 8 Gaps: 0

US-10-656-394A-8 (1-1032) x US-10-656-394A-16 (1-3674)

QY 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerIysAla 20  
 Db 9 ATGGCGGAGAGCGTCTGCTGAGCATGGCGAGGCTCGTGGTGGCAGTGCCTCAGCAAGGCC 68  
 QY 21 AlaSerAlaAlaAappGluThrSerLeuLeuGlyValGluIleAspIleThrTyr 40  
 Db 69 GCCTCTGCGCTGCAATGAGCAGGAGCTCTCTGCTGGCGTGGAGAGGACATCTGGTAT 128  
 QY 41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetIlys 60  
 Db 129 ATCAAGATGAGTAAACAAATGACAGGCATCTCTGCTGGCGTGGAGAGGACATCTGGTAT 188  
 QY 61 LysAspGluLeuLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGlu 80  
 Db 189 AAAGATGAACATTAAGAAGTTTGGCGAGCAATACGTGACCTGCTGATGACATGAA 248  
 QY 81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100  
 Db 249 GATTCCTTGTGAATTAAGTCCATATTTGAAGCCAAACCTATTTCTGTCAGTTGGTG 308  
 QY 101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGlu 120  
 Db 309 AAACCTTAGAGAGCCCGGATCGCTATCCGATATCAACCTCAACCTCAACCTCAACCTCAAC 368  
 QY 121 GluValSerSerArgAsnThrArgTyrSerLeuValLysProIleSerSerGlyThrGlu 140  
 Db 369 GAAGTGTAGTACAGCAACACAGCTCAATTTAGTCGAGCCTATTTCTCGGCGCAGAG 428  
 QY 141 IleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAspGlu 160  
 Db 429 GATGACATGGATTCCTATGACAGAGACATTCGCAATCAATCAGCTCGCAATTTGTGATGA 488

QY 161 AlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThrAsn 180  
 Db 489 GCTGAGCTTGTGGGTTTTCTGACTCCAAGAAGAGCTGCTTGAATATGATGATACCAAT 548  
 QY 181 AlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLysThr 200  
 Db 549 GCTAATGATGCTCCGGCCCAAGGTAATCTGTGTGTGTGGATGGTGGTGGTGGTGGTGGT 608  
 QY 201 AlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsn 220  
 Db 609 GCTCTTTTCGAGGAGATCTTTTGAAGCGAAGAGACATTTAGGAAGAACTTCCTCTTGC 668  
 QY 221 AlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArg 240  
 Db 669 GCTTGGATTTACAGTGTGCACATCTTTTCACAGGATTTAGTACTTAAAGATATGATACGC 728  
 QY 241 GlnLeuLeuGlyProSerSerLeuAspGlnLeuLeuGlnGluGlnGlyLysValVal 260  
 Db 729 CAACCTTCTGGTCCCAAGTTCTCTGGAATCAACTCTTGCATGAATTCGAAGGGAAGGTGGT 788  
 QY 261 ValGlnValHisLeuSerGluTyrLeuIleGluGluLeuLysGluLysArgTyrPhe 280  
 Db 789 GTGCAAGTACATCATCTTTCTGAGTACCTGATAGAAGAGCTCAAGAGAGAGGAGTACTTT 848  
 QY 281 ValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAlaPhe 300  
 Db 849 GTTGTCTTAGATGATCTATGATGATTTTACATGATTTGGAATTTGGAATTTGCAATTT 908  
 QY 301 ProLysAsnLeuLysLysGlySerArgIleValIleThrThrArgAsnValAspLeuAla 320  
 Db 909 CCTAAGAACCAATTAAGAGGAGGAGTGCATAGTAATTAACCACTCGAATTTGTATGATCG 968  
 QY 321 GluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAspAla 340  
 Db 969 GAGAAGTGTGCCACAGCCTCACTGGTGTACCACTTGTATTTCTTCAGATGAACGATGCC 1028  
 QY 341 IleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsn 360  
 Db 1029 ATTTCAATGCTACTGAGAAAACCAATTAATAATCATGAAGACATGGAATCAATATAAAT 1088  
 QY 361 MetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeu 380  
 Db 1089 ATGCAAAAGATGTTGAAACGATTTGAAATAAATGTTGCTGCTGCTACCAATTTAGCAAT 1148  
 QY 381 ThrIleGlyValAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyrGluHis 400  
 Db 1149 ACAATAGAGAGCTGTGCTTGCACATAAACAAGTGTGAGATGGAGAAATTTCTATGAACA 1208  
 QY 401 LeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgArgMetValThrLeu 420  
 Db 1209 CTTCCTTTTCAGAACTAGAAAATAAACCCAGCCTGGAAGCTTTTTCAGAGAGAAATGCTG 1268  
 QY 421 GlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePhePro 440  
 Db 1269 GGTTCACCAACCTACATCCCATCTGAACCAACCTGCTTTTGTATCTTAGATCTTTCTCT 1328  
 QY 441 GluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheVal 460  
 Db 1329 GAGGATTTTGAATACAAAGGAATCGCTCTAGTAGTAGATGATGAGAGAGGAGGTTGTT 1388  
 QY 461 ArgProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeuIle 480  
 Db 1389 AGACCAAGGTTGGGATGAGCTAGAGATGCGGAGAAAGTACTTCTTATGAGCTAATC 1448  
 QY 481 AsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArg 500  
 Db 1449 AACCGAAGTATGATTCACAGATCAAGAGTGGGCACAGCAGGAAAAAATAAGACTTGTGCA 1508  
 QY 501 IleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGlnAsnPheValLeu 520  
 Db 1509 ATCCATGATATCATCGTGATTCACAGTTTCAATCTCGACAGAGAAAAATTTTGTATTATTA 1568  
 QY 521 LeuProMetGlyAspGlySerAspValGlnGlnAsnThrArgHisIleAlaPheHis 540

Db 1569 TTACCAATGGGAGATGGCTCTGATTAGTTTACAGAAAACACTCGCCACATAGCATTCAT 1628  
Qy 541 GlySerMetSerCysLeuThrGlyLeuAspTrpSerIleLeuArgSerLeuAlaIlePhe 560  
Db 1629 GGGAGTATGTCCTGCAAAACAGGATGGATGGAGCATATTTCGATCATTAGCATTTT 1688  
Qy 561 GlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArg 580  
Db 1689 GGTGACAGACCCAGAGCTAGCACATGCAGTTGTTCAGATCAATTTGAGGATGTACGG 1748  
Qy 581 ValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAla 600  
Db 1749 GTCTTGGATCTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCACCGTATTGCA 1808  
Qy 601 LeuLeuCysHisLeuLysThrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuPro 620  
Db 1809 TTGTTGTGCCACTTGAAATACCTTCAGTATTGGATATTTCGTATCCATATATTCACTTCCC 1868  
Qy 621 ArgSerIleGlyLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAla 640  
Db 1869 AGATCATTTGGTAAACTACAGGCTTACAGCTTTGAACATGTCAAGCACATACATTGCA 1928  
Qy 641 AlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGln 660  
Db 1929 GCACCTACCAAGTGAGATCAGTAAACTCAATGTCTGCATACTCTTCGTTGTATAAGAG 1988  
Qy 661 PheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIleThrSerThrIleCys 680  
Db 1989 CTTGAATTTGACAACTTTAGTCTAAATCACCATGAAGTGCAATACTAACCAATATGC 2048  
Qy 700 LeuProLysValPheThrProLeuValSerArgAspArgAlaLysGlnIleAlaGlu 700  
Db 2049 CTGCTTAAGTATTACACCTTTAGTTCGCGATAATCGTCAAAACAAATTTGCTGAA 2108  
Qy 701 LeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLysGly 720  
Db 2109 TTTTCACTGGCCACCAAAAGTTTCGGTCTGAATCATTCGGTGAAGGTACCCAAAGA 2168  
Qy 721 IleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgThrSerSer 740  
Db 2169 ATAGGTAACTTCGGAGACTTACAGCTTCAGAGTATGTAGATATCAGCGGCGACAGTAGT 2228  
Qy 741 ArgAlaIleLysGlnLeuGlyClnLeuSerLysLeuArgLysLeuGlyValThrAsn 760  
Db 2229 AGAGCAATCAAAAGCTGGGGCAGTTAAGCAAGTTGAGGAAATTAGCTGTGATACAAA 2288  
Qy 761 GlySerThrLysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLeu 780  
Db 2289 GGCTCGCAAAAGGAAATGTAAGATCTTTATGACGCAATGAGAGCTCTCTCCCTC 2348  
Qy 781 GlnSerLeuHisValAspAlaAlaGlyLysSerAspGlyGlyThrLeuGluCysLeuAsp 800  
Db 2349 CAATCTCTCTATATGAATCTCGCTATTATCAGATATTTGAACACTTTGAGTGCCTAGAT 2408  
Qy 801 SerIleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGluGlu 820  
Db 2409 TCTATTTCATCT 2468  
Qy 821 MetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeuArgSerLys 840  
Db 2469 ATGCTTAACCTGGATTCAGCAGCTCACTCACCTGAGAGAGTTTCAACTTATGAGATGATAA 2528  
Qy 841 LeuLysGluGlyThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetValLeuHis 860  
Db 2529 CTAAGGAGGTAAAAACATGCTGTACTCTGGGCACTGCGCACTCATCTGTTCTCTCTCTCT 2588  
Qy 861 LeuTyrArgAsnAlaTyrLeuGlyLysLeuValPheLysThrGlyAlaPheProAsn 880  
Db 2589 CTTTATCATTAATCTTATCTTGGGAGAGCTAGTATTTCAAAACGGGAGCATTTCCCAAT 2648  
Qy 881 LeuArgThrLeuTrpIleTyrGluLeuAspGlnLeuArgGluIleArgPheGluAspGly 900

Db 2649 CTTAGAACACTTGTGATTTTCAATTTGGATCAGCTAAGAGAGATCAGATTTTGAGACGCG 2708  
Qy 901 SerSerProLeuLeuGluLysIleGluIleGlyGluCysArgLeuGluSerGlyIleThr 920  
Db 2709 AGCTCACCCAGCTTGGAAAAAGATAGAAATCTCTTGTGCAAGTTGGAATCAGGGATTATT 2768  
Qy 921 GlyIleIleHisLeuProLysLeuLysGluIleProIleArgTyrGlySerLysValAla 940  
Db 2769 GGTATCATCTACCTTCCAGGCTCAAGGAGATTTCACTTTGAATACAAAGATTAAGTGCT 2828  
Qy 941 GlyLeuGlyGlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeuLeuMet 960  
Db 2829 AGGCTTGGTCAAGTGAAGGAGAGTGAACACACACACCCAAATCGCCCGCTGCTGCAATG 2888  
Qy 961 TyrSerAspArgTyrHisAspLeuGlyValAlaGluAlaGluGlySerSerIleGluVal 980  
Db 2889 GACAGTGACCGAGGATCAGCCTGGGGCTGAAGCGGAGGATCTTCTATAGAGTG 2948  
Qy 981 GlnThrAlaAspProValProAspAlaGluGlySerValThrValAlaValGluAlaThr 1000  
Db 2949 CAAACAGCAGATCTCTTCTGATGCCCAAGGATCAGTCACTGTAGCAGTGAAGCAAG 3008  
Qy 1001 AspProLeuProGluGlnGluGlyGlySerSerGlnSerGlnValIleThrLeuThrThr 1020  
Db 3009 GATCCCTTCCCGAGCAGGAGGAGAGCTCGCAGTCCGAGGTGATCAGTTGACGAGCG 3068  
Qy 1021 AsnAspSerGluGluIleGlyThrAlaGlnAlaGly 1032  
Db 3069 AATGATAGCAAGAGATAGGACAGCTCAAGCTGGC 3104

## RESULT 7

US-10-352-179-83

; Sequence 83, Application US/10352179

; Publication NO. US20040006788A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Guo-liang

; APPLICANT: Liu, Guifu

; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pl

; FILE REFERENCE: 2727/04108

; CURRENT APPLICATION NUMBER: US/10/352,179

; PRIOR FILING DATE: 2003-01-27

; PRIOR APPLICATION NUMBER: 60/352,106

; PRIOR FILING DATE: 2002-01-25

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 83

; LENGTH: 76272

; TYPE: DNA

; ORGANISM: Oryza minuta

US-10-352-179-83

Alignment Scores:

Pred. No.:	0	Length:	76272
Score:	4753.00	Matches:	938
Percent Similarity:	96.8%	Conservative:	14
Best Local Similarity:	95.4%	Mismatches:	31
Query Match:	90.2%	Indels:	0
DB:	6	Gaps:	0

US-10-656-394A-8 (1-1032) x US-10-352-179-83 (1-76272)

Qy 40 TyrIleLysAspGluLeuLysThrMetClnAlaPheLeuArgAlaGluLeuMetLys 59  
Db 62063 TATATCAAGATGAGCTATAAACCGATGCAAGCATCTCTTAGCTGCTGAACCTTATGAA 62122  
Qy 60 LysLysAspGluLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyrAspIle 79  
Db 62123 AAGAAGATGAATTAAGGTTGGCAGAGCAATACGTGACCTGTCTATGACATT 62182  
Qy 80 GluAspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeu 99  
Db 62183 GAAGATTCCCTTGATGAATTAAGGTCCATATTGAAGCCAAACCCCTATTTCGTGAGTTG 62242

Qy 100 ValLysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgVal 119  
Db 62243 GTGAAATCTCAGAGAACGCCCAATTCCTATCCGATATCCACACCTTAATAACAGAGTT 62302  
Qy 120 GluGluValSerSerArgAsnThrArgTyrSerLeuValLysProLysSerGlyThr 139  
Db 62303 GAAGAGTGTAGTACAGGAGAACACACGCTACAGTTTGTAGTCAAGCCTATTTCTCTGGCACA 62362  
Qy 140 GluIleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAsp 159  
Db 62363 GAGATTGACATGGATTCTTATCGAAGACATTCGTAAATCAGTCAGCTCCCAATGGAT 62422  
Qy 160 GluAlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThr 179  
Db 62423 GAAGCTGAGCTTGTGGTTTCTGACTCCAAGAAAGGTTGCTTGAATGATCGATACC 62482  
Qy 180 AsnAlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyLysLeuGlyLys 199  
Db 62483 AATGCTTAATGATGGTCCGCCCAAGTAATCTGTGTGTGGATGGGTGGTTAGGCAG 62542  
Qy 200 ThrAlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCys 219  
Db 62543 ACAGCTCTTCGAGGAAGATCTTTGAAGCGAAGACATAGGAAGAACTTCCCTTGC 62602  
Qy 220 AsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLysAspMetIle 239  
Db 62603 AATGCTTGGATTACAGTGTCAATCATTTTCAAGGATGGATGAGTCTCAAGATATGATA 62662  
Qy 240 ArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuLeuGlnGlyLysVal 259  
Db 62663 CGCCAACTCTAGTCCCAATCTCTGAAACACTCTTCGAGAAATGGCAAGGAGTG 62722  
Qy 260 ValValGlnValHisLeuSerGluTyrIleLeuGluLeuLysGluLysArgTyr 279  
Db 62723 GTGGTCAAGTATACATCATCTTTCTGAGTACCTGTAGAGAGCTCAAGGAGAGAGGTAC 62782  
Qy 280 PheValValLeuAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAla 299  
Db 62783 TTTGTATTCTAGATGATCTAGTATTTTACATGATGGAATGGATGGAATGGAATGGA 62842  
Qy 300 PheProLysAsnLysLysGlySerArgIleValIleThrArgAsnValAspLeu 319  
Db 62843 TTTTCTTAAGAACAAATAAGAGGCGAGTCGAATAGTAAATCACTCGAATGTGTATCTA 62902  
Qy 320 AlaGluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAsp 339  
Db 62903 GCGGAGAGTGTGCCACAGCTCACTGTGTACCACTTGATTTCTTCAGATGAACGAT 62962  
Qy 340 AlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLys 359  
Db 62963 GCCATTAACATTGTCTAAGAAACAAATAAATCAATGAACATGGAATCAATATAA 63022  
Qy 360 AsnMetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIle 379  
Db 63023 AATATGCAAAAGATGGTTGAACCAATTTGTAAATAATGTGGTGTCTACCAATAGCATA 63082  
Qy 380 LeuThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyrGlu 399  
Db 63083 CTTACAAATAGGAGCTGTGTGCTCAACTAAACATGTGTGAGAAATGGAATTTCTATGAA 63142  
Qy 400 HisLeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgArgMetValThr 419  
Db 63143 CAGCTTCTCTAGAACTAGAAATAAACCAAGCTTGAAGCTTTGAGGAATGGTGACC 63202  
Qy 420 LeuGlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePhe 439  
Db 63203 CTAGGTTACACACCACTACCACTCCATCTGAAACCATGCTTTTGTATCTAAGATATCTT 63262  
Qy 440 ProGluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPhe 459  
Db 63263 CCTGAGATTTTGAATCAAAAGGAATCTGTGTGTAGTGTAGATGATGATGCAAGGGTTT 63322  
Qy 460 ValArgProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeu 479

Db 63323 GTTAGACCCGAGTTGGGATGACGACTAAGGATTCGGAGAAAGTTACTTTAATAGCTA 63382  
Qy 480 IleAsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCys 499  
Db 63383 ATCAGCCGAAGTATGATTCAACGATCAAGAGTGGCATATCAGCAAAAATTAAGACTGT 63442  
Qy 500 ArgIleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGluAsnPheVal 519  
Db 63443 CGAATCCATGATATCATCCGATATCACAGTTTCAATCTCGAGACAGGAAATTTGTA 63502  
Qy 520 LeuLeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPhe 539  
Db 63503 TTGTTACCAATGGGAGATGGCTCTGATTTAGTTTCAAGAAAACACTGCCACATAGCATTC 63562  
Qy 540 HisGlySerMetSerCysLeuThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIle 559  
Db 63563 CATGGAGTATGTCCTGCAAAACAGGATGGATTTGGAGCATTAATTCGATCATTAGCTATT 63622  
Qy 560 PheGlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeu 579  
Db 63623 TTTGTTGACAGACCCCAAGCTTAGCACATGTCAGTTTGTCTAGATCAATTTGAGGATGTTA 63682  
Qy 580 ArgValLeuAspLeuLysValThrPheLeuIleThrGlnLysAspPheAspArgIle 599  
Db 63683 CGGGTCTTGGATCTTTGAAGATGTGACATTTCTTAATCACTCAAAAGATTTTCGACCGTATT 63742  
Qy 600 AlaLeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeu 619  
Db 63743 GCATTTGTTGCCACTTGAATACTTCAGTATTGGATATTCGTCATCATATATTCACATT 63802  
Qy 620 ProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIle 639  
Db 63803 CCCAGATCCATTGGTAAACTACAGGCGCTACAACTTTGAACATGCTGGAACATACATT 63862  
Qy 640 AlaAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGly 659  
Db 63863 GCAGCACTACCAAGTGAGATCAGTAACCTCCAATGCTCGCATATCTTCTGTTGATGATA 63922  
Qy 660 GlnPheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIle 679  
Db 63923 AAGTTGTTTATGACACTTTAGTCTAAACCCCAATGAAGTGAATTAATTAACCAATA 63982  
Qy 680 CysLeuProLysValPheThrProLeuValSerArgAspArgAlaLysGlnIleAla 699  
Db 63983 TGCTCTGCCTAAAGTATTACACACTTTAGTTAGTGGCGATGATCGTGCATAAACAATGCT 64042  
Qy 700 GluLeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLys 719  
Db 64043 GAATTGCACTGGCCACCACCAAGTTGCTGTCTGAAATCAATTCGGTGTGAAGGTACCCAAA 64102  
Qy 720 GlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgArgThrSer 739  
Db 64103 GGAATAGGTAGTTCGAGACTTCAGGTTCTAGAGTATCTAGATATCAGCGGACCACT 64162  
Qy 740 SerArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrThr 759  
Db 64163 AGTAGAGCAATCAAGAGCTGGGCGCACTTAAGCAAGTTGAGGAATTTAGTGTGATAACA 64222  
Qy 760 AsnGlySerThrLysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSer 779  
Db 64223 AAAGGCTGCACAAAGGAATAATGTAGATTAATTTATGAGCCATTTGAGAAAGCTCTCTCC 64282  
Qy 780 LeuGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLeu 799  
Db 64283 CTCCAATCTCTATGTGAATGCTGCGCTTATTAATTAATCAGATATTGAACAACATTTGAGTGCCTA 64342  
Qy 800 AspSerIleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGlu 819  
Db 64343 GATTCATTTTCACT 64402  
Qy 820 GluMetProAsnTrpIleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeuArgSer 839



Db 64403 GAGATGCCCTAACTGGATTGACGACCTCACTCACTGAGAGAGATCTACTATTATTGAGGAGC 64462  
Qy 840 LysLeuLysGluGlyLysThrMetLeuLeuLeuGlyAlaLeuProhenLeuMetValLeu 859  
Db 64463 AAACCTAAAGGAAGGATTAACCATCTGATACCTTTGGGGCATTTGCCCAACCTCATGTGCTTT 64522  
Qy 860 HisLeuTyArgAsnAlaTyLeuGlyGluLysLeuValPheLysThrGlyAlaPhePro 879  
Db 64523 TAATCTTAATGGATGCTTACCTTGGGGAGAGCTAGTATTCAAACGGGAGCATTCCTCA 64582  
Qy 880 AsnLeuArgThrLeuTrpIleTyGluLeuAspGlnLeuArgGluLeuArgPheGluAsp 899  
Db 64583 AATCTTAGAACACTTCGTATTACCAATTCGATCAGCTAAGACAGATGAGATTCGAGGAT 64642  
Qy 900 GlySerSerProLeuLeuLysLeuValLeuGlyGluLysLeuValLeuGlyGluLysLeuVal 919  
Db 64643 GGCAGCTACCCCTCTTGGAAAGATAGAAATCTCTTGGCAGGTTGGATCAGGGATT 64702  
Qy 920 ThrGlyIleLeuHisLeuProLysLeuLysGluLeuProIleArgTyGlySerLysVal 939  
Db 64703 ATTGGTATCAATTCACCTTCCCAAGCTCAAGGAGATTCACCTGAATACAAAGTAAAGTG 64762  
Qy 940 AlaGlyLeuGlyGlnLeuGlyGluValAsnAlaHisProAsnArgProValLeuLeu 959  
Db 64763 GCTAGGCTTGGTCACTGGAGGAGAGAGTGAACACACCCCAATCGCCCGCTGCTGCGA 64822  
Qy 960 MetTySerAspArgTyArgHisAspLeuGlyAlaGluLeuGlySerSerIleGlu 979  
Db 64823 ATGGACAGTGACCGAAGGATCACGACCTGGGGGCTGACCGAGGATCTTCTATAGAA 64882  
Qy 980 ValGlnThrAlaAspProValProAspAlaGluGlySerValThrValAlaValGluAla 999  
Db 64883 GTGCAACACGACAGATCTCTGTTCTGTCGCGAAGGATCAGTCACTGATGACGTGGAAGA 64942  
Qy 1000 ThrAspProLeuProGluGlnGluGlySerSerGlnSerGlnValIleThrLeuThr 1019  
Db 64943 ACGGATCCCTTCCCGACGAGGAGGAGAGCTGCGAGTGGCAGTGATCAGGTTGAGC 65002  
Qy 1020 ThrAsnAsp 1022  
Db 65003 ACGAACGAT 65011

## RESULT 8

US-10-437-963-37316  
; Sequence 37316, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 37316  
; LENGTH: 4596  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_41056C.1  
US-10-437-963-37316

## Alignment Scores:

Pred. No.: 0 Length: 4596  
Score: 4397.50 Matches: 862  
Percent Similarity: 97.3% Conservative: 11

Best Local Similarity: 96.1% Mismatches: 17  
Query Match: 83.5% Indels: 7  
DB: 7 Gaps: 3

US-10-656-394A-8 (1-1032) x US-10-437-963-37316 (1-4596)

Qy .135 IleSerSerGlyThrGlu-----IleAspMetAspSerTyAlaGluAspIleArgAsn 152  
Db 4 GTGGCACTGGCAACCACTGCTTACCAATAGATTCCTATGCAGAAAGACATTCGCAAT 63  
Qy 153 GlnSerAlaArgAsnValAspGluAlaGluLeuValGlyPheSerAspSerLysLysArg 172  
Db 64 CAATCAGCTCGAAATGTGGATGAAGCTGAGCTTGTGGGTTTCTGACTCCAAAGAAAGG 123  
Qy 173 LeuLeuGluMetIleAspThrAsnAlaAsnAspGlyProAlaLysValIleCysValVal 192  
Db 124 CTGCTTGAATGATCGATACCAATGCTAATGATGGTCCGGCCCAAGATTAATCTGTGTTGT 183  
Qy 193 GlyMetGlyGlyLeuGlyLysThrAlaLeuSerArgLysIlePheGluSerGluGluAsp 212  
Db 184 GGGATGGGTGGTTTAGGCAAGACAGCTCTTTTCGAGGAAGATCTTTTGAAGCGAAGAAC 243  
Qy 213 IleArgLysAsnPheProCysAsnAlaTrpIleThrValSerGlnSerPheHisArgIle 232  
Db 244 ATTAGGAAGAACTTCCCTTCCCAATGCTTGGATTCAGTGTACATCATCTTTCACAGGAT 303  
Qy 233 GluLeuLysAspMetIleArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuLeu 252  
Db 304 GAGCTACTTAAAGATATGATACGCCAACTTCTTGGCCCGCAGTTCTCTGGATCAACTCTTG 363  
Qy 253 GlnGluLeuGlnGlyLysValValGlnValHisHisLeuSerGluTyLeuIleGlu 272  
Db 364 CAAGAATTGCAAGGAGAGGTGGTGGTGAAGTACATCATCTTTCGAGTACTGTATAGAA 423  
Qy 273 GluLeuLysGluLysArgTyPheValValLeuAspAspLeuTrpIleLeuHisAspTrp 292  
Db 424 GAGCTCAAGGAGAGAGGTACTTGTGTCTTAGATGATCTATGGAATTTTACATGATGG 483  
Qy 293 AsnTrpIleAsnGluIleAlaPheProLysAsnAsnLysLysGlySerArgIleValIle 312  
Db 484 AATTGGATTAATGAATTTGCAATTTCTTAAGAACATTAAGAGGGCAGTCAATAGTAAATA 543  
Qy 313 ThrThrArgAsnValAspLeuAlaGluLysCysAlaThrAlaSerLeuValTyHisLeu 332  
Db 544 ACCACTCGGAATGTTGATCTTGGGAGAGAGTGGCCACAGCTCACTGGTGTACCACCTT 603  
Qy 333 AspPheLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArgTyThrAsnLysAsnHis 352  
Db 604 GATTTCTTGCAGATGAACGATGCCATTAACATTTGCTACTGAGAAAAACAATAAATAATCAT 663  
Qy 353 GluAspMetGluSerAsnLysAsnMetGlnLysMetValGluArgIleValAsnLysCys 372  
Db 664 GAAGACATGGNATCAATAATAAATAATGCAAAAGATGGTTGAACGAATTTGTAATAAATGT 723  
Qy 373 GlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrLysGlnValSer 392  
Db 724 GGTGCTCTACCATTTAGCAATTAATAAGAGGCTGTGCTTGAACCTAAACAGGTGCA 783  
Qy 393 GluTrpGluLysPheTyGluHisLeuProSerGluLeuGluIleAsnProSerSerLeuGlu 412  
Db 784 GAATGGGNGAATTTCTATGAACACTTCTTCAAGAACTAGAAATAAACCAGGCTGAA 843  
Qy 413 AlaLeuArgArgMetValThrLeuGlyTyAsnHisLeuProSerHisLeuLysProCys 432  
Db 844 GCTTTGAGGAGAAATGGTGACCTTCTAGGTTTGAATCAACCACTTCACTTCCATCTGAAACCATG 903  
Qy 433 PheLeuTyLeuSerIlePheProGluAspPheGluIleLysArgAsnArgLeuValGly 452  
Db 904 TTTTGTATCTAAGTATCTTCTTCTGAGGATTTTGAATCAAAAGGATTCGCTAGTAGGT 963  
Qy 453 ArgTrpIleAlaGluGlyPheValArgProLysValGlyMetThrThrLysAspValGly 472  
Db 964 AGATGGATAGCAGAGGGGTTTGTAGACCAAGAGGTTGGGATGACGACTAAAGATGTGCGA 1023



```
QY 473 GluSerTyrPheAsnGluLeuLeuAsnArgSerMetIleGlnArgSerArgValGlyIle 492
DB 1024 GAAAGTTACTTTAAATGAGCTAATCAACCGAAGTATGATTCAACGATCAAGAGTGGGCATA 1083
QY 493 AlaGlyValIleValThrCysArgIleHisAspIleIleArgAspIleThrValSerIle 512
DB 1084 GCAGGAAATAATTAAGACTTGTGCAATTCATGATATCATCCGATATCAAGTTCAATC 1143
QY 513 SerArgGlnGluAspPheValLeuLeuProMetGlyAspGlySerAspLeuValGlnGlu 532
DB 1144 TCAGACACAGAAAAATTTTGTATTTGTTACCAATGGGAGATGGCTCTGATTTAGTTTCAGGAA 1203
QY 533 AsnThrArgHisIleAlaPheHisGlySerMetSerCysValThrGlyLeuAspTrpSer 552
DB 1204 AACCTCGCCACATAGCAATTCATGGGAGTATGTCCTGCACAAACAGAGTTGATTTGGAGC 1263
QY 553 IleIleArgSerLeuAlaIlePheGlyAspArgProLysSerLeuAlaHisAlaValCys 572
DB 1264 ATTATTCGATCATTTAGCTATTTTGTGTCACAGACCCCAAGAGTCTAGCACATCGAGTTGT 1323
QY 573 ProAspGlnLeuArgMetLeuArgValLeuAspLeuGluAspValThrPheLeuIleThr 592
DB 1324 CAGATCAATTCAGGATGTTACGGGTCTTGGATCTTGAAGTGTGACATCTTAATCACT 1383
QY 593 GlnLysAspPheAspArgIleAlaLeuLeuCysHisLeuLysTyrLeuSerIleGlyTyr 612
DB 1384 CAAAAAGATTTTCGACCATATTTGCTGTTGTCACCTTGAATATCTTGAGTATTCGATAT 1443
QY 613 SerSerSerIleTyrSerLeuProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeu 632
DB 1444 TGTCTCATCATATATTCATCTCCAGATCCATTTGGTAAACTACAGGGCCCTACAAACTTTG 1503
QY 633 AsnMetProSerThrTyrIleAlaLeuProSerGluIleSerLysLeuGlnCysLeu 652
DB 1504 AACATGCCGACACATACATTTGCAGCACTACCAAGTGAGATCAGTAAATCTCCAACTGTG 1563
QY 653 HisThrLeuArgCysIleGlyGlnPheHisTyrAspAsnPheSerLeuAsnHisProMet 672
DB 1564 CATACTCTTCGTTGTATAGGACAGTTTCATATGACAACTTTTGTATGCTAAACCAACCAATG 1623
QY 673 LysCysIleThrAsnThrIleCysLeuProLysValPheThrProLeuValSerArgAsp 692
DB 1624 AAGTGATAACTAAACACAAATATGCTGCTAAAGTATTCACACTTTTAGTTAGTCGCAT 1683
QY 693 AspArgAlaLysGlnIleAlaGluLeuHisMetAlaThrLysSerCysTrpSerGluSer 712
DB 1684 GATCGTGCAAAACAAATTTGCTGAATTCACATGGCCACCAAAAGTTGCTGGTCTGAATCA 1743
QY 713 IleGlyValLysValProLysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyr 732
DB 1744 TTCGGTGTGAAGGTACCCAAAGGAATAGGTAAGTTGCGAGACTTACAGGTTCTAGAGTAT 1803
QY 733 ValAspIleArgThrSerSerArgAlaIleLysGluLeuGlyGlnLeuSerLysLeu 752
DB 1804 GTAGATATCAGCGGACCAAGTAGTAGAGCAATCAAGAGCTGGGGCAGTTAAGCAAGCTG 1863
QY 753 ArgLysLeuGlyValThrAsnGlySerThrLysGluLysCysLysIleLeuTyrAla 772
DB 1864 AGGAATTTAGTGTGCACAAACAAACGGGTTCGACAAAGGAAATGTAAGTACTTTATGCA 1923
QY 773 AlaIleGluLysLeuSerSerLeuGlnSerLeuHisValAspAla-----AlaGly 789
DB 1924 GCCATTTGAAGACTCTCTTCTCCATCTCTCCATGTCGATGTCGTGTTATTTCTCAGGT 1983
QY 790 IleSerAspGlyGlyThrLeuGluCysLeuAspSerIleSerSerProProLeuLeu 809
DB 1984 ATTATTT-----GGAAACACTTGAAGTCTAGATTTCTATTTCTCTCTCTCTCTCTCTA 2037
QY 810 ArgThrLeuValLeuAspGlyIleLeuGluGluMetProAsnTrpIleGluGlnLeuThr 829
DB 2038 AGGACACTCAGGTTGAATGGGAAGTCTTTGAAGAGATGCTTAACCTGGATTCAGCAGCTCACT 2097
```

```
QY 830 HisLeuLysLysIleTyrLeuLeuArgSerLysLeuLysGluGlyLysThrMetLeuIle 849
DB 2098 CACCTGGAAGAGTTTCGACTTTTACCGAGAGGTAAACATAAGGAGGTAAACCATGCTGATA 2157
QY 850 LeuGlyAlaLeuProAsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGlu 869
DB 2158 CTTGGGGCATTTGCCAACCTCATGGTCCCTTATCTTATCGGAATGCTTACCTTTGGGGAG 2217
QY 870 LysLeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyrGluLeu 889
DB 2218 AAGCTAGTATTTCAAAACGGGAGCATTTCCCAAAATCTTTAGAACACTTTGTTATTACGAATTG 2277
QY 890 AspGlnLeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGlu 909
DB 2278 GATCAGCTAGAGAGATCAGATTTTAGAGAGCGGACGCTCACCCCTCTTGGAAAAGATAGAA 2337
QY 910 IleGlyGluCysArgLeuGluSerGlyIleThrGlyIleIleHisLeuProLysLeuLys 929
DB 2338 ATAGGCAAGTGCAGGTTGGAAATCTGGGATTTATTTGGTATCATTTCACTTTCCAAAGCTCAAG 2397
QY 930 GluIleProIleArgTyrGlySerLysValAlaGlyLeuGlyGlnLeuGluGlyGluVal 949
DB 2398 CAGATTTCCATATACATACAGAGTAAAGTGGCTGGGCTTGGTCAGCTGGAGGAGAGTG 2457
QY 950 AsnAlaHisProAsnArgProValLeuLeuMetTyrSerAspArgTyrHisAspLeu 969
DB 2458 AACACACACCAATCGCCCGTGTCTGCTTAATGTACAGTACCGAAGGTATCACGACCTG 2517
QY 970 GlyAlaGluAlaGlySerSerIleGluValGlnThrAlaAspProValProAspAla 989
DB 2518 GGGGCTGAGCCGAGAGATCTTCTATAGAAAGTGCAACAGCAGATCTCTGTTCTGTATGCC 2577
QY 990 GluGlySerValThrValAlaValGluAlaThrAspProLeuProGluGlnGlyGlu 1009
DB 2578 GAAGGATCAGTCACTGTAGCAGTGGGAAGCAACGAGTCCCTTCCCGAGCAGGAGGAGAG 2637
QY 1010 SerSerGlnSerGlnValIleThrLeuThrThrAsnAspSerGluGluIle 1026
DB 2638 AGCTCGCAGTCGCGAGGATCACGTTGACAGCAATGATAGGAATCGTCTTA 2688
```

## RESULT 9

```
US-10-656-394A-11
; Sequence 11, Application US/10656394A
; Publication No. US20040210957A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: Cloning and Characterization of the
; FILE OF INVENTION: broad-spectrum resistance gene P12
; FILE REFERENCE: 035718/252062
; CURRENT APPLICATION NUMBER: US/10/656,394A
; CURRENT FILING DATE: 2003-09-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 2997
; TYPE: DNA
; ORGANISM: Oryza minuta
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(2997)
US-10-656-394A-11
```

```
Alignment Scores:
Pred. No.: 0 Length: 2997
Score: 4241.50 Matches: 861
Percent Similarity: 84.8% Conservative: 17
Best Local Similarity: 83.2% Mismatches: 49
Query Match: 80.5% Indels: 108
DB: 8 Gaps: 5
```

US-10-656-394A-8 (1-1032) x US-10-656-394A-11 (1-2997)

QY 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20

|||||  
1 ATGGCGGAGACGGTGTGAGCATGGCGAGGTGCTGGTGGGAGCGCCATCAGCAAGGCC 60  
21 AlaSerAlaAlaAlaAspGluThrSerLeuLeuGlyValGluLysAspIleTyr 40  
61 GCCTCGCGCGTGGCGAGCAGCAGCCTCTCTGCTGGCGTGGAGAGACATCTGGTAC 120  
41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysLys 60  
120 ----- 120  
61 LysAspGluLeuLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGlu 80  
120 ----- 120  
81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100  
121 -----TTGTTTAGACATGGTGT 138  
101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGlu 120  
138 ----- 138  
121 GluValSerSerArgAsnThrArgTyrSerLeuValLysProIleSerSerGlyThrGlu 140  
139 -----GGACGGTCGAATGGTGGGCGCTGTTGTAGGTATGGTGCATCTGGCAACCG 189  
141 -----IleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnVal 158  
190 TCATGCTTAGCAATAGATTCCTATGCAGAGACATCCCATCAATCAGCTCGAATGTG 249  
159 AspGluAlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAsp 178  
250 GATGAAGCTGAGCTGTTGGTGTCTGACTCCCAAGAAAGCGCTGCTTGAATGATCGAT 309  
179 ThrAsnAlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGly 198  
310 ACCAATGCTTAATGATGGTCCGCGCAAGGTAATCTGTGTGTGGATGGGTGTTAGGC 369  
199 LysThrAlaLysSerArgLysIlePheGluSerGluLeuAspIleArgLysAsnPro 218  
370 AAGACAGCTCTTTTCGAGGAAGATCTTTGAAAGCGAAGACAGACATAGGAAGAACTTCCT 429  
219 CysAsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLysAspMet 238  
430 TGCATGCTTGGATTACAGTGTCACAATCATTTACAGGATGAGCTACTTAAAGATAG 489  
239 IleArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuLeuGlnIleGlnGlyLys 258  
490 ATACGCCAATCTTGGCCCCAGTTCTCTGGATCACTCTTGCAAGAAATGGCAAGGAAG 549  
259 ValValValGlnValHisIleSerGluTyrLeuIleGluLeuLysGluLysArg 278  
550 GTGGTGGTGCAGATCATCATCTTTCTGAGTACCTGTATAGAGAGCTCAAGGAGGAAGG 609  
279 TyrPheValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIle 298  
610 TACTTGTGTTCTAGATGATCTATGGATTTTACATGATTGGAATTGGATAAATGAAT 669  
299 AlaPheProLysAsnLysLysGlySerArgIleValIleThrThrArgAsnValAsp 318  
670 GCATTTCTTAAGAACAAATAGAGGGCAGTCAATAGTAAATACCACTTGGATGTTGAT 729  
319 LeuAlaGluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsn 338  
730 CTTGGCGGAGAGTGTGCCACAGCTCACTGGTGTACCACTTGATTTCTTTCGAGATGAAC 789  
339 AspAlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsn 358  
790 GATGCCATACATTTGCTACTGAGAAAAAATAATAAATATCATGAAGACATGGGAATCAAT 849  
359 LysAsnMetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAla 378  
|||||

850 AAAAATATGCAAAAGATGGTTGAACGAATTTGTAATAATAATGTGGTCTACCATTAGCA 909  
379 IleLeuThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyr 398  
910 ATACTTCAATAGGAGCTGTGCTTGAACATAACAGGTGTGAGATGGAGAAATCTTAT 969  
399 GluHisLeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgArgMetVal 418  
970 GAACACCTTCTCTCAGAACTAGAAATAAACCACCAAGCTCGAAAGCTTTGAGGAGAAATGGTG 1029  
419 ThrLeuGlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIle 438  
1030 ACCCTAGGTATCAACACCACTTACCATCCATCTGAAACCAATGCTTTTGTATCTAAGTATC 1089  
439 PheProGluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGly 458  
1090 TTTCTGAGGATTTTGAATCAAAAGGAATCGTCTAGTAGGTAGATGATGATGATGATG 1149  
459 PheValArgProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGlu 478  
1150 TTTGTAGACCAAAAGGTGGGATGACGACTAAGGATGTGCGAGAAAGTTTACTTTAATGAG 1209  
479 LeuIleAsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThr 498  
1210 CTATCAACCGAAGTATGATTTCAACGATCAAGAGTGGCATAGCAGGAAAAAATTAAGACT 1269  
499 CysArgIleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGluAsnPhe 518  
1270 TGTGCAATTCATGATATCATCCGTGATATCACAGTTTCAATCTCGAGACAGGAAAAATTTT 1329  
519 ValLeuLeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAla 538  
1330 GTATTGTTTACCATTTGGAGATGGCTCTGATTAGTTTCAGGAAAAACACTGCCACATAGCA 1389  
539 PheHisGlySerMetSerCysLysThrGlyLeuAspTrpSerIleIleArgSerLeuAla 558  
1390 TTCCATGGGAGTATGTCCTGCAAAACAGGATTTGGATTGGAGCATTTATTCGATCATAGCT 1449  
559 IlePheGlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMet 578  
1450 ATTTTGTGTGACAGACCAAGAGCTAGCACATGTCAGTTGTTCAGATCAATTTGAGGATG 1509  
579 LeuArgValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArg 598  
1510 TTACGGGTCTTGGATCTTTGAAGATGTGACATTTCTAATCACTCAAAAGATTTTCGACCGT 1569  
599 IleAlaLeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSerSerIleTyrSer 618  
1570 ATTTGATTTGTGTCACCTTTGAAATACCTTGAGTATTTGGATTTTCGTCATCATATATCA 1629  
619 LeuProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyr 638  
1630 CTTCCAGATCCATTTGGTAACTACAGGGCTTACAAACTTTGAACATGCGAGCACATAC 1689  
639 IleAlaAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIle 658  
1690 ATTTGACGACACTACCAAGTGAGTCACTTGAATCTTCAATGCTCGATACTCTTGTGTAGT 1749  
659 GlyGlnPheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThr 678  
1750 AGAAAGTTTGTCTCTGCAACTTTTAGTCTTAAACCAACCACTTGAAGTGAATCAATCAACA 1809  
679 IleCysLeuProLysValPheThrProLeuValSerArgAspArgAlaLysGlnIle 698  
1810 ATATGCTGCTTAAAGTATTCACACCTTTTAGTTAGTTCGGATGATGATCGTCAATATCAAT 1869  
699 AlaGluLeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValPro 718  
1870 GCTGATTTGCATATGGCCACCAAAAGTTGCTGGTATAAATCATTTTCGTTGAGGTATCCC 1929  
719 LysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgArgThr 738  
1930 AAAGGAATAGGTAAAGTTCGAGACTTACAGGTCTTAGAGTATGTAGATATCAGGCGGAC 1989  
|||||

Qy 739 SerSerArgAlaIleIysGluLeuGlyGlnLeuSerIysLeuArgIysLeuGlyValThr 758  
Db 1990 AGTAGTAGAGCAATCAAGAGCTGGGGCAGTTAAAGCAAGCTGAGGAATATAGGTGTGATG 2049  
Qy 759 ThrAsnGlySerThrIysGluIysCysIysValIleLeuTyraAlaIleGluIysLeuSer 778  
Db 2050 ACAATGGCTGCANAGGAAATATGAAGTACTTTGTGAGCCATTGAGAGCTCTCT 2109  
Qy 779 SerLeuGlnSerLeuHisValAspAlaIleGlyIleSerAspGlyIleThrLeuGluCys 798  
Db 2110 TCCCTCCAAATATCTCTATGAATGCTGCAGGAATCTCAGATGCTGGAACATCTGAGTGC 2169  
Qy 799 LeuAspSerIleSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeu 818  
Db 2170 CTAGATTCTATTCT 2229  
Qy 819 GluGluMetProAsnTrpIleGluGlnLeuThrHisLeuIysIysIleTyLeuLeuArg 838  
Db 2230 GAAGAGATGCTAACTGGATTGAGCAGCTCACTCACTGGAAGAAGATCTACTATTATGAGG 2289  
Qy 839 SerIysLeuIysGluIysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetVal 858  
Db 2290 AGCAACTAAGAGAGGTAACCACTGCTGATCTTGGGGCATTGCCAACCTCATGCTC 2349  
Qy 859 LeuHisLeuTyraAsnAlaTyrlleuGlyGluIysLeuValPheIysThrGlyAlaPhe 878  
Db 2350 CTTGATCTTTATCGGAAGCTTACCTTGGGGAGAGCTAGTATTCAAAAACAGAGCATTC 2409  
Qy 879 ProAsnLeuArgThrLeuTrpIleTyrlleuLeuAspGlnLeuArgGluIleArgPheGlu 898  
Db 2410 CCAATCTTAGAACACTTTCGATTTCAGATTTCGATCAGCTAAGAGATTAGATTGAG 2469  
Qy 899 AspGlySerProLeuLeuGluIysIleGluIleGluCysArgLeuGluSerGly 918  
Db 2470 GACGGCAGCTCGCCCGAGTTGGAAGAGATAGAAATCAGATTCTGCAGGTTGGAATCAGGG 2529  
Qy 919 IleThrGlyIleIleHisLeuProIysLeuIysGluIleProIleArgTyrlleGlySerIys 938  
Db 2530 ATTATTGGTATTATCCACCTTCCAAAGCTCAAGAGATTTCATCTGGATCAGAAAGTAA 2589  
Qy 939 ValAlaGlyLeuGlnLeuGluIysGluValAsnAlaHisProAsnArgProValLeu 958  
Db 2590 GTGGCTGGCTGCTCAGCTGAGGAGAGAGTGGCCACACACCAAAATCACCCCGTGTG 2649  
Qy 959 LeuMetTyraAsnArgTyrlleAspLeuGlyAlaGluAlaGluSerSerIle 978  
Db 2650 CGAAGAGGAGGAGCCGAGTGTATCAGCACTTCTGTCGACCCGAGAGATCCCTCTGT 2709  
Qy 979 GluValGlnThrAlaAspProValProAspAlaGluIysSerValThrValAlaValGlu 998  
Db 2710 GAA-----GTGGAA 2718  
Qy 999 AlaThrAspProLeuProGluGlnGluIysSerSerGlnSerGlnValIleThrLeu 1018  
Db 2719 GCAACGGATCCCTCCAGAGCAGGAGGAGAGC----- 2754  
Qy 1019 ThrThrAsnAsp-SerGluGluIleGlyThrAlaGlnAlaGly 1032  
Db 2755 -----TCGACGGAAGAGATAAGCACAGCTCAAGCTGGT 2788

## RESULT 10

US-10-437-963-2483  
; Sequence 2483, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 2483  
; LENGTH: 2982  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_102251C.1  
US-10-437-963-2483

Alignment Scores:  
Pred. No.: 0 Length: 2982  
Score: 3664.50 Matches: 733  
Percent Similarity: 81.6% Conservative: 76  
Best Local Similarity: 73.9% Mismatches: 122  
Query Match: 69.6% Indels: 61  
DB: 7 Gaps: 2

US-10-656-394A-8 (1-1032) x US-10-437-963-2483 (1-2982)

Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerIysAla 20  
Db 178 ATGGCGGAGAGCGGTGCTGAGCATGGCGAGGTCGCTGCTGGCGAGTGCCATCAGCAAGGCC 237  
Qy 21 AlaSerAlaAlaAlaAspGluThrSerLeuLeuGlyValGluIysAspIleTrpTy 40  
Db 238 ACCTCTGGCGGGCCCATGAGCGGCGCTCTACTCGGCGTCCAGAGGACATCTGGTAT 297  
Qy 41 IleIysAspGluLeuIysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetIysLys 60  
Db 298 ATCAAAGATGAGCTGAAACCAATGCAAGCGTTCCTACGAGCTGCTGCAAGTTATGAAGA 357  
Qy 61 LysAspGluLeuLeuIysValTrpAlaGluGlnIleArgAspLeuSerTyraAspIleGlu 80  
Db 358 AAAGATGAGCTCTTAAAGGTTTGGCGAGAACATGACATAGTACGTGCTGCTTATGACATTGA 417  
Qy 81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100  
Db 418 GATTCCTTTCAGCAATTCAGGTCATATTTAGAGGCCAAATCTGTTTATCAGATGCTG 477  
Qy 101 LysLeuArgGluArgHisAglleAlaIleArgIleHisAsnLeuIysSerArgValGlu 120  
Db 478 AAGCTCAGAAAGCGCCATCTGATAGCTACCCAAATCCGTAACCTCAAATCAAGAGTTGAA 537  
Qy 121 GluValSerSerArgAsnThrArgTyrlleSerLeuValIysProIleSerSerGlyThrGlu 140  
Db 538 GAAGTGAGTAGCAGAAACTCAGCTACAAATTTAGTCAAACTATTTCATCCAGCAATGAG 597  
Qy 141 IleAspMetAspSerTyraAlaGluAspIleArgAsnGlnSerAlaArgAsnValAspGlu 160  
Db 598 GATGACATGGATGTTTACGAGAGACATTCGTAATCAGTCACTCACTAGCAATGATGAA 657  
Qy 161 AlaGluLeuValGlyPheSerAspSerIysLysArgLeuGluMetIleAspThrAsn 180  
Db 658 ACTGAGCTTGTGGGGTCTCTGACTCTAG----- 687  
Qy 181 AlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyLeuGlyLysThr 200  
Db 687----- 687  
Qy 201 AlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsn 220  
Db 687----- 687  
Qy 221 AlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuIysAspMetIleArg 240  
Db 688-----ATAAGGATTGAGCTACTACTCAAGATATGATACGG 720

Qy		241	GlnLeuLeuGlyProSerSerLeuAspGlnLeuLeuGlnGluVal	260
Dd		721	CRAATTCCTAGGTTCCCAATTCCACTGGATCAAGTCTTGCAAGAATTCGACGGCGAAATGTGGT	780
Qy		261	ValGlnValHisHisLeuSerGluTyrrLeuIleGluLeuLysGluLysArgCyrPhe	280
Dd		781	GTGCCAATAACCTCATCTTCGTACTACTTTGAAAAAGCTCAAGGAAGAAGAGATATTTT	840
Qy		281	ValValLeuAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAlaPhe	300
Dd		841	GTGTGCTTGATGATCATGTCTTAGATGCATGSAATCGAATTAATGATATTGCATTT	900
Qy		301	ProLysAsnAsnLysLysGlySerArgIleValIleThrThrArgAsnValAspLeuAla	320
Dd		901	CCTAAGATAACAATAAGGCGATCGGATGTAGTAACACACAGAGATGTGTGTAGCC	960
Qy		321	GluLysCysAlaThrAlaSerLeuValTyrrHisLeuAspPheLeuGlnMetAsnAspAla	340
Dd		961	GAGAGTGTACCACCACTTCCCCTAGTCTACCATCTTGAACACTTGCAGATGAATGATGCC	1020
Qy		341	IleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsn	360
Dd		1021	ATAACTTTGCTACTGAGAAAAAACAAATAGAACACATGAGGACATGGGAAACAAAAT	1080
Qy		361	MetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeu	380
Dd		1081	ATGCAAAAAATAGTGTGAACAAATGTAAATAGTGTGGCGCTCTACCATAGCGATACTT	1140
Qy		381	ThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyrrGluHis	400
Dd		1141	ACAATAGGAGCTGTGTTGGCAACTAAACAAGTTTTAGAAATGGAGAAATTTTATAACAG	1200
Qy		401	LeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgArgMetValThrLeu	420
Dd		1201	CTTCCCTTCAGAACTTGAAAGCAACCCAGCCTTCAAGCTTTGAGAGAGAATGGTACCCTT	1260
Qy		421	GlyTyrrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrrLeuSerIlePhePro	440
Dd		1261	GSCTACACCACTGCCATCTCATCTGAAATCATGCTTTTGTACCTAAAGTATCTTCCCT	1320
Qy		441	GluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheVal	460
Dd		1321	GAGGAATTTGAGATCAAAAGAGTCGCTGTGTAGACAGATGGATTCGAGAGGGGTGTGT	1380
Qy		461	ArgProLysValGlyMetThrThrLysAspValGlyLysSerTyrrPheAsnGluLeuIle	480
Dd		1381	AGAGCCNAGTTGGATGACGACGAGAGATTTGGGCAGTGTACTTTAATAGACTAATC	1440
Qy		481	AsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyIleIserThrCysArg	500
Dd		1441	AACCCGAAGTATGATTCAAAGATCAAGATGGGCATAGAGGAAAAATTAAGAGTGGCGA	1500
Qy		501	IleHisAspIleIleArgAspIleThrValSerIleSerArgGlnAsnPheValLeu	520
Dd		1501	GTCCATGATATCATGCGTGATATCACATTTCAATCTCTAGAGAGAGAACTTTGTATTC	1560
Qy		521	LeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHis	540
Dd		1561	TTACAGATGCATGATGGCTCCAATCTAGCACAGAAAAACATCGCCACATAGCATTCGAT	1620
Qy		541	GlySerMetSerCysLyvThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIlePhe	560
Dd		1621	GGAGCATGTCTCTGCAANACAGATTCGATTTGAGCATTTTCGATCTTACCTATTTTTT	1680
Qy		561	GlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArg	580
Dd		1681	GGTGACAGACCCCAATAATCTAGCACACATATTGTTCAAAATAAATTCAGAGTGTACGG	1740
Qy		581	valLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAsnArgIleAla	600
Dd		1741	GTGTGGATCTTGAAGATGTGAAGTTTTTAATCACAAAAAGATTTTCAACAATATAGCA	1800
Qy		601	LeuLeuCysHisLeuLysTyrrLeuSerIleGly-----TyrrSerSerSerIleTyrrSer	618

Db 2881 CGTATGAGAGGAGCCAGAGCTGTCTCAGACCTGAGAGCGGATGCCAAGGATCAGCTGTA 2940

Qy 979 GluValGlnThrAlaAspProValProAspAlaGlu 990

Db 2941 GAAATGAAGCAACGAGCGCCCTCCCTGAGCCGAG 2976

## RESULT 11

US-10-352-179-90

; Sequence 90, Application US/10352179

; Publication No. US20040006788A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Guo-liang

; TITLE OF INVENTION: Procedures and Materials for Conferring Disease Resistance in Pla

; FILE REFERENCE: 22727/04108

; CURRENT APPLICATION NUMBER: US/10/352,179

; CURRENT FILING DATE: 2003-01-27

; PRIOR APPLICATION NUMBER: 60/352,106

; NUMBER OF SEQ ID NOS: 97

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 90

; LENGTH: 3220

; TYPE: DNA

; ORGANISM: Oryza minuta

US-10-352-179-90

## Alignment Scores:

Pred. No.: 2,96e-292 Length: 3220

Score: 3205.50 Matches: 667

Percent Similarity: 74.4% Conservative: 133

Best Local Similarity: 62.0% Mismatches: 202

Query Match: 60.8% Indels: 76

DB: 6 Gaps: 11

US-10-656-394a-8 (1-1032) x US-10-352-179-90 (1-3220)

Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerIleVala 20

Db 1 ATGCGGATACAGTACTCAGCAATTCGAAGTCCCTGCTGGGAGAGTCTGTGAAGCAAGTT 60

Qy 21 AlaSerAlaAlaAspGluThrSerLeuLeuGlyValGluIleAspIleTyr 40

Db 61 GCTTCGTTGCCGAGACAAAGATGATCATGCTGCTGGAGTGCAGAGGAGATATGTTTC 120

Qy 41 IleIleAspGluLeuIleThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetIleIys 60

Db 121 ATCAAGATGAGCTACAAACGATACAGCATTTTGTGATGCTGCCGAA--GCATCAAG 177

Qy 61 LysAspGluLeuIleValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGlu 80

Db 178 AAAAGCATACTATTGAAGTTTGGGTGCAGCAAGTAAGGATCTTCTCATGACATTGAA 237

Qy 81 AspSerLeuAspGluPheIleValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100

Db 238 GATTGCTTGATGAATTTACAGTTCATGCTGGGCGCAAACTTGTGAGCGGAGTTGATG 297

Qy 101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisLeuIleIysSerArgValGlu 120

Db 298 AACCTAAAGAGTCGCATCGGATTCGATCCAGATCCGCAATCTCAGGCAAGAATTGAA 357

Qy 121 GluValSerSerArgAsnThrArgTyrSerLeuValIys--ProIleSerSerGlyThr 139

Db 358 GAAGTAAGCAGCTAGGAGACATACGCTACAACTTAATAGGAATGACCTTCACTCCGACCACT 417

Qy 140 GluIleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAsp 159

Db 418 ACTGATGAGAGGAATTTATTATGAGACATCTCGAACCAATAAGCTAACCAACTGAG 477

Qy 160 GluAlaGluLeuValGlyPheSerAspSerIleIysArgLeuLeuGluMetIleAspThr 179

Db 478 GAAGCTGATCTGTGGGTTTTTCTGGACCCCAAAAGAGAGTTGCTTATCTTATAGATGTC 537

Qy 180 AsnAlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLys 199

Db 538 CATGCCAATGACGGACCTACAAAAGTTGTATGTTGTCGATATGGGTGGGTAAG 597

Qy 200 ThrAlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCys 219

Db 598 ACTACTATTGCGAAGGAAATTTATGAAGCAAGAGGACATTCGAAAGATTTTCTTGC 657

Qy 220 AsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIle 239

Db 658 TGTGCTTGAGTACTGTTTTCACAGTCTCTTTGTTAGGTTGGAAGTACTCAAGGATTTGATG 717

Qy 240 ArgGlnLeuGlyProSerSerLeuAspGlnLeuLeuGlnGluLeuGlnGlyLysVal 259

Db 718 GTGAAACTTTTGGAGAGGAGTACTGAAAGAGCGCTGAGAGACTCGAAGGGAAG--- 774

Qy 260 ValValGlnValHisLeuSerGluTyrIleGluLeuGluLeuLysGlyLysArgTyr 279

Db 775 GTTCCACAAAGTAGAGACCTCGCCAGCTACTCAGGACAGAGTAAATGAAAGAGGTAC 834

Qy 280 PheValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAla 299

Db 835 TTTGTTGCTGTGATACGCTGAGTACAGATTCATGGAATGGATTATAGTAGTTGCC 894

Qy 300 PheProLysAsnAsnLysLysGlySerArgIleValIleThrThrArgAsnValAspLeu 319

Db 895 TTCCCTAGAAAATAACAATAAAGGAGCGCGGTGATAGTAACAACAAGAGATGTTGCTTA 954

Qy 320 AlaGluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAsp 339

Db 955 ACTAAGGAGTGTACTTCTGAAATGCTTATCTACAGCTTAAACCCCTAGAAATAAAGTAT 1014

Qy 340 AlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLys 359

Db 1015 GCAAAAGAGTTGCTTCTACGGAAGCAATAAAGCAATAGGAGATATGGAAGTGTATAA 1074

Qy 360 AsnMetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIle 379

Db 1075 AGATGAGTGACATTAATAAATAAATAAAGAGTGTGGCTATTATACCGTGGCTATA 1134

Qy 380 LeuThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpIleLysPheTyrGlu 399

Db 1135 CTCACAAATAGGAGCGTCTTCCACCAAGAGATAAGAGAGTGGGAAACTTTTATAGT 1194

Qy 400 HisLeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgMetValThr 419

Db 1195 CAGATACCTTCAGAGCTTGAGAGCAACCCAAACCTTGAAGCAATGAGAGGATAGTGACC 1254

Qy 420 LeuGlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePhe 439

Db 1255 CTAAAGTACAACTACTTACCGTCTCATCTTAAAGCAATGCTTTTGTATCTAAGCATATT 1314

Qy 440 ProGluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGlyPhe 459

Db 1315 CCTGAGGATTTTGAATTAATAGGAACCGTCTGGTAAATAGATAGTGGACAGGGGTTT 1374

Qy 460 ValArgProLysValGlyMetThrThrLysAspValGlyLysSerTyrPheAsnGluLeu 479

Db 1375 ATTAAGCTAGGACTAATATGACTATTATGAAGATGTTGGGAAAGTTACTTTAAAGACTT 1434

Qy 480 IleAsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCys 499

Db 1435 ATCAACCGCTAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1494

Qy 500 ArgIleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGluAsnPheVal 519

Db 1495 CGAGTCCACGACATCATCGTGTATTTACAAATTTCTGATTTCTAGAGAGAAATTTTACA 1554

Qy 520 LeuLeuProMetGlyAspGlySerAsnLeuValGlnGluAsnThrArgHisIleAlaPhe 539

Db 1555 CTCATTACCGGATGCTGACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1614

Qy 540 HisGlySerMetSerCys---LysThrGlyLeuAspTrpSerIleIleArgSerLeuAla 558

Db 1615 CACGGAGTAAATGCTCTGAAACAAAGCTTGAGACTGAGCAATATACGGTCAATAACT 1674  
Qy 559 ILePheGlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMet 578  
Db 1675 ATGTTTGGTGGAGAGTCCGAGAACTAGAGCAATTCAGTTGTTGTTTCATCTCAGTTCAGGATG 1734  
Qy 579 LeuArgValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArg 598  
Db 1735 TTACGGGCTTTGGATCTTAAACAGATGCAACAATTTCTATCACACAAATGATGTGCAAC 1794  
Qy 599 ILeAlaLeuLeuCysHisLeuLysThrLeuSerIleGlyTyr-----SerSerSe 615  
Db 1795 ATAGTGCTCTGTGCCACTTGAATACCTATGCAATTAAGATACAGATACCGTTTCAACATA 1854  
Qy 615 rIleTyrSerLeuProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetPr 635  
Db 1855 TATTTATTCATCTCCAAATCCATAGTACGACTGCACTGCTGCGACAAATTTGGACTTGGG 1914  
Qy 635 oSerThrTyrIleAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLe 655  
Db 1915 TCAGACGTACATTTCAACATGCGCACTCAGATTACTAA-CTTCGGAGTCTCCGAGCT 1973  
Qy 655 uArgCysIleGlnPheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIl 675  
Db 1974 TCGATGCAATGAAGAATATTTCTTCTTCTTAAACA-----ACATATTT 2018  
Qy 675 eThrAsnThrIleCysLeuProLysValPheThrProLeuValSerArgAspAspAl 695  
Db 2019 AACTTAACACATATGCTGCGCATGATATTCACACCTTTCGTTAGTACTCGGATCGTTC 2078  
Qy 695 alyeGlnIleAlaGluLeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyVa 715  
Db 2079 TGAACAAATGCTAAATTTGACATGCGCAACCAAGGCTTCCGTTCAAAATCAAAATGGTGT 2138  
Qy 715 llyValProLysGlyIle---GlyLysLeuArg-AspLeuGlnValLeuGluTyrVala 734  
Db 2139 CAAGTACCAAAAGGATATGTAATTAATAAAACTCGACTTACAAATATGAGGATGTTGG 2198  
Qy 734 spIleArgArgThrSerArgAlaIleLysLeuGluGlnLeuSerLysLeuArgL 754  
Db 2199 ATATTAGAGGACTAGCAGTAGCAATCAAGAGTTGGGGCAGTTAAGCAAGCTGAGGA 2258  
Qy 754 yLeuGlyValThrThrAsnGlySerThrLysLysCysLysIleLeuTyrAlaAl 774  
Db 2259 AATTATGTGTGTAACAAAGGATCCAAAGGAAATGTGAGATCTCTATACAGCTA 2318  
Qy 774 leGluLysLeuSerSerLeuGlnSerLeuHisValAspAlaAlaGlyLysSerAspGly 794  
Db 2319 TCCAGAGCTCTGTTTCTTCAATCTCTCCATGTGAATGCTGTGGGATTTTCAGGTATTG 2378  
Qy 794 lyThrLeuGluCysLeuAspSerIleSerProProLeuLeuArgThrLeuVal 814  
Db 2379 GAACACTTCAGTGTATGATCTTATTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2438  
Qy 814 euAspGlyLeuLeuGluLeuMetProAsnTrpIleGluGlnLeuThrHisLeuLysLysI 834  
Db 2439 TGAATGGAAGCTTTGAGGAGATGCTTAACCTGGATTGAGCAGCTCAGCACCTGATGAGT 2498  
Qy 834 leTyrLeuLeuArgSerLysLeuLysGlyLysThrMetLeuIleLeuGlyAlaLeuP 854  
Db 2499 TCAACTTATGAGAGGAGCAAACTAAAGAGGTAACCAATGTGTACTTCGGCGGTGC 2558  
Qy 854 roAsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyLysLeuValPheL 874  
Db 2559 CCAACCTCATGCTCTTTATCTTCTTCAATGCTTACCATGGGAGAGCTAGTATTCA 2618  
Qy 874 yThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyrGluLeuAspGlnLeuArg 894  
Db 2619 AAATGGGAGCAATCCCAAAATCTTAGAACATTTTCGATTTTACAAATTTGAGCAGCTAAG 2678  
Qy 894 luIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGluGlyCysA 914

Db 2679 AGATTAGATTGAGGAGCGGAGCTCAATCTTGTGAAAGAGTAAATATT-CAG---G 2734  
Qy 914 rgLeuGluSerGlyIleThrGlyIleIleHisLeuProLysLeuLysGluIleProIleA 934  
Db 2735 GGTGGAAATCAGGAGATTGTTGGTATCATTTCACTTTCAAGGCTCAAGGAGATTTCAC 2794  
Qy 934 rgTyrGlySerLysValAlaGlyLeuGlyGlnLeuGluGlyValAsnAlaHisProA 954  
Db 2795 GATACGGAATGAATGAGTGGCTTGGTTCAGCTGGAGGAGAGTGGCGACACACCCAA 2854  
Qy 954 snArgProValLeuLeuMetTyrSerArgArgTyrHisAspLeuGlyAlaGluAlaG 974  
Db 2855 ATCACCCCGTGTCCGAATGAGGAGGAGCGAAGTGCATCAGCACCTTCTTGTGACGCG 2914  
Qy 974 luGlySerSerIleGluValGlnThrAlaAspProValProAspAlaGluGlySerVal 994  
Db 2915 AAGGATCCCTCTTGA----- 2931  
Qy 994 hrValAlaValGluAlaThrAspProLeuProGluGlnGluGlyGluSerSerGlnSerG 1014  
Db 2932 -----GTGGAAGCAACAGATCCTGT-----GAGAGCTCACAGTTGC 2967  
Qy 1014 lnValIleThrLeuThrThrAsnAsp----- 1022  
Db 2968 AGGTGATCATCGTTGCAACAGCAAGAGTAAAGCACTTAAGCTGTGT 3128  
Qy 1022 ----- 1022  
Db 3028 CTGTTTATCTCTTGTGAGATCGATGATTTTAACCTACCCCTTCTCTCTCGTTT 3087  
Qy 1023 -----SerGluGluIleGlyThrAlaGlnAlaGly 1032  
Db 3088 CTTAACCTAACAGCAAGAGTAAAGCACTTAAGCTGTGT 3128

## RESULT 12

US-10-656-394A-5  
; Sequence 5, Application US/10656394A  
; Publication No. US20040210957A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang et al.  
; TITLE OF INVENTION: Cloning and Characterization of the  
; TITLE OF INVENTION: broad-spectrum resistance gene P12  
; FILE REFERENCE: 035718/252062  
; CURRENT APPLICATION NUMBER: US/10/656,394A  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 4147  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1983)  
US-10-656-394A-5

Alignment Scores:  
Pred. No.: 1,68e-285 Length: 4147  
Score: 3136.00 Matches: 676  
Percent Similarity: 63.0% Conservative: 126  
Best Local Similarity: 53.1% Mismatches: 200  
Query Match: 59.5% Indels: 274  
DB: 8 Gaps: 11

US-10-656-394A-8 (1-1032) x US-10-656-394A-5 (1-4147)

Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20  
Db 1 ATGCGGATACAGTACTCAGCAATTCGAAAGTCCCTCGTGGAGAGTCTGTGAAGAGTT 60  
Qy 21 AlaserAlaAlaAlaAspGluThrSerLeuLeuGlyValGluLysAspIleTrpTyr 40  
Db 61 GCTTCGGTCCCGCAGACAAGATGATCATGTCTGCTGGAGTGCAGAGGAGATATGTTTC 120



41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysLys 60  
121 ATCAAAGATGAGCTACAAACGATACAAAGCATTTTGAATGCTGCCGAA---GCATCAAG 177  
61 LysAspGluLeuLysValTTPAlaGluGlnIleArgAspLeuSerTyrAspIleGlu 80  
178 AAAACCATCTATTGAAGTTTGGTGCAGCAGTAGTAGGATCTTCTATGACATCGAA 237  
81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100  
238 GATTCCTTGTATGAATTTACAGTTTCATGTGGCAGCAAAACCTTGTCCAGGCAGTTGAT 297  
101 LysLeuArgGluArgHisArgIleAlaIleArgIleHisAsnLeuLysSerArgValGlu 120  
298 AAGCTAAGGATCGCCATCGGATTCGATCCAGATCCGCAATCTCAGACAGAAATGAA 357  
121 GluValSerSerArgAsnThrArgTyrSerLeuValLysPheProIleSerSerGlyThrGlu 140  
358 GAAAGTAAGCATTAGCAACATACGCTACAACTTAATAGAGATGACCTCACCTGCACCACT 417  
141 IleAspMetAspSerTyrAlaGluAspIleArgAsnGlnSerAlaArgAsnValAspGlu 160  
418 GATGAGAGAAATTTATTATGGAAGACATTCGCATCAATCAATGAGTAAACATCGAGAA 477  
161 AlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThrAsn 180  
478 GCTGATCTGTGGGTTTTTCTGGACCCMAAGAGAGTGTCTTGATTTATAGATGTCAT 537  
181 AlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLysThr 200  
538 GCCAAGGACGACCTACAAAGTTGTATGTTGTGGTATGGGTGGTGGTGGTAAAGACT 597  
201 AlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCysAsn 220  
598 ACTATTGCAAGGAAATTTATGAAGCAAGAGAGACATTTGCAAGAAATTTCTTGCTGT 657  
221 AlaThrIleThrValSerGlnSerPheHisArgIleGluLeuLysLysAspMetIleArg 240  
658 GCTTGATTTACTGTTTACAGTCTTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 717  
241 GlnLeuLeuGlyProSerSerLeuAspGlnLeuLeuGlnGluGlnGlyLysValVal 260  
718 AAACTTTTGGAGAGGAAGTACTGAAAGCGCGAGAGAACTCGAAGGGAAG---GTT 774  
261 ValGlnValHisLysLeuSerGluTyrLeuIleGluLeuLysGlyLysArgTyrPhe 280  
775 CCACAGTAGATGACCTTGCAGCTACCTCAGACAGAGATTACATGAAGAGAGTACTTT 834  
281 ValValLeuAspAspLeuTTPileLeuHisAspTTPAsnTTPileAsnGluIleAlaPhe 300  
835 GTTGTGCTTGATGACGTGTGGAGTACAGATTCATGGAATGGATTAATAGTATTGCTTC 894  
301 ProLysAsnAsnLysGlySerArgIleValIleThrArgAsnValAspLeuAla 320  
895 CCTAGAATAACAAAAAAGGAGCGCGGTGATAGTAAACAAAGAGATGTTGGCTTAGCT 954  
321 GluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAspAla 340  
955 AAGAAGTGTACTTCTGAATTTGCTTATCTACCAGCTTAAACCCCTAGAAATAAATATGCA 1014  
341 IleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsn 360  
1075 ATGAGTGACATTATACTAAATAGTAAGAGAGTGTGGTATTTACCGCTGGCTATATCTC 1134  
381 ThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTyrGluLysPheTyrGluHis 400  
1135 ACAATAGAGCGCGTCTTCCACCAAGAGATAGAGAGAGTGGGAACTTTTATATAGTCAG 1194

401 LeuProSerGluLeuGluLeuLeuLeuProSerLeuGluAlaLeuArgArgMetValThrIleu 420  
1195 ATACCTTTGAGAGCTTGAGAGCAACCCAAACCTTGAAGCAATGAGAAGGATAGTAGCCCTA 1254  
421 GlyTyrAsnHisLeuProSerHisLysLysProCysPheLeuTyrLeuSerIlePhePro 440  
1255 AGTTACACATCTATTACGTTCTATCTTAAGCAATGCTTTTGTATCTAAGCATATTTCCT 1314  
441 GluAspPheGluIleLysArgAsnArgLeuValGlyArgTTPileAlaGluGlyPheVal 460  
1315 GAGGATTTTGAATTAATAGCAACCGTCTGTGTAATAGATGATGTCAGAGGGGTATT 1374  
461 ArgProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeuIle 480  
1375 AAACCTAGGACTAATATGACTATTGAGATGTTGGGAAGAGTTACTTTTAAAGAACTTATC 1434  
481 AsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArg 500  
1435 AACCGTAGCATGATTGAGTCATCAAGAGCGGTATACGAGGAGATTTTAAAGAGCTCGA 1494  
501 IleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGlnAsnPheValLeu 520  
1495 GTCCATGACATCATGCTGATATTAATTCATTTCTAGAGAAGAAAATTTTCACTC 1554  
521 LeuProMetGlyAspGlySerAspLeuValGlnGlnAsnThrArgHisIleAlaPheHis 540  
1555 TTACCCGATGGCACTGACTATGATGTAGTACATGGGAACACTCGGCACATAGCATTTTAC 1614  
541 GlySerMetSerCys---LysThrGlyLeuAspTTPSerIleIleArgSerLeuAlaIle 559  
1615 GGGAGTAGGTATGCTCTGAAACAAGCTTGGACTGGACATTTATACGCTTAACTATG 1674  
560 PheGlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeu 579  
1675 TTTGGTGAGAGGTCCTGAGAACTAGAGCATCAGTTGCTCATCTCAGTTGAGGATGTA 1734  
580 ArgValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIle 599  
1735 CGGCTCTTGATCTAATAGATGCAAAATTTCTATCACACAAAATGATGTGCAACAATA 1794  
600 AlaLeuLeuCysHisLeuLysTyrLeuSerIleGly-----TyrSerSerSer 615  
1795 GTGCTCTTGTGCCACTTGAATACCTACGATTCGACATGCAAGATACAGATCCGTTACCATAT 1854  
616 IleTyrSerLeuProArgSerIleGlyLysLeuGlnGlnLysLeuAsnMetPro 635  
1855 ATTTATTTCACTTCCACATCCATAGCTAGATGCTGTCAGACATTCGAGCTGGGT 1914  
636 SerThrTyrIleAlaAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeu 655  
1915 CAGACGTACATTTCAACACTGCAACTCAGATTTACTAA---CTTCGGAGTCTCCGTAGCCTT 1973  
656 ArgCysIleGlyClnPheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIle 675  
1974 CGATGATGAAGAA-----TATTTTCTTCTTCTTTAAGA-----ACATATTTA 2018  
676 ThrAsnThrIleCysLeuProLysValPheThrProLeuValSerArgAspAspArgAla 695  
2019 ACTAACACATTTATGCTGCCATGATATTACACCTTTTCGTTAGTACCTCGGATCGTTCT 2078  
696 LysGlnIleAlaGluLeuHisMetAlaThrLysSerCysTTPSerGluSerIleGlyVal 715  
2079 GAAACAATTTGCTAAATGACATGCGCCACCAAGGCTTCGTTCCAAATCAAAATGGGTGTC 2138  
716 LysValProLysGlyIleGlyLysLeuArg----- 725  
2139 AAGGTACCAAAAGATATGTAAGTTGAGACATTACAGAGGATTCGTACGGTCCAGCA 2198  
725 ----- 725  
2199 GGTGTGACCGGGCGGTACTGGTACCGCGGTAACAAACCCATCTAACCGTTGAATCCG 2258  
725 ----- 725

Db 2259 GGATGGGTAGGATCGGAGAGAAAGATGACGAAGGGTGGATGAGGAGTACCTGTTTCG 2318  
QY 725 ----- 725  
Db 2319 AGTCGTCTTCCCGCGCGCGCGGCTGGAGTACCTGTTTCGAGTCTGTCGTTCCGG 2378  
QY 725 ----- 725  
Db 2379 TGGCGGCGAGAGCAACAAGGAGCGCGCGCGCGGAGAGGATAAAGTCCGGCGGAG 2438  
QY 725 ----- 725  
Db 2439 CCGGAG 2498  
QY 725 ----- 725  
Db 2499 CGGCGGAG 2558  
QY 725 ----- 725  
Db 2559 CCAGCTAGTCTAGGTTTCGAGCGCGCGCGAGTCCAAACCATCTATTGACGCGAGTTACT 2618  
QY 725 ----- 725  
Db 2619 CTTTACCTTCCAACTCTCTCTCATGCGGTATCACCTAAGGAGACATTTTGTGACCG 2678  
QY 725 ----- 725  
Db 2679 TCGGTACACGCAACATCAGCGCTTGGATCAGCGCGAGATCCACCGCGAGATTTGGTA 2738  
QY 726 ----- 726  
Db 2739 CGCTCGGTACGTTGGACAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2798  
QY 735 eArgThrSerArgAlaIleLysGluLeuGlnLeuSerLysLeuArgLysLe 755  
Db 2799 TAGAAGGACTAGAGTAGAGCAATCAAGAGATGGGGCAGTTAAGCAGCTGAGGAAT 2858  
QY 755 uGlyValThrAenGlySerThrLysGluLysCysLysIleLeuTyAlaAlaIleG 775  
Db 2859 ATGTGTGTAAACAAAGGATCCACAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2918  
QY 775 uLysLeuSerSerLeuGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyL 795  
Db 2919 GAAGCTCTGTCTTACAACTCTCCATGTGAATGCTGGGATTTTCAGGTATGGAAC 2978  
QY 795 rLeuGluCysLeuAspSerLysSerSerProProLeuLeuArgThrLeuValLeuAs 815  
Db 2979 ACTTCAGTGTATAGATCTATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3038  
QY 815 pGlyLeuLeuGluMetProAenThrLleGluGlnLeuThrHisLeuLysLysIleTy 835  
Db 3039 TGAAGTCTTGGAGAGATGCTTAACCTGATGAGCAGCTCAGCAGCTGATGAAGTTCAA 3098  
QY 835 rLeuLeuArgSerLysLeuLysGluLysThrMetLeuLeuLeuGlyAlaLeuProAs 855  
Db 3099 CTTATGGAGGAGCAACATAAGAGAGTAAACCATGTTGGTACTTTCGGCGGTGCCAA 3158  
QY 855 nLeuMetValLeuHisLeuTyArgAenAlaTyLeuGluLysLeuValPheLysTh 875  
Db 3159 CCTCATGTGCTTTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3218  
QY 875 rGlyAlaPheProAenLeuArgThrLeuThrLleTyGluLeuAspGlnLeuArgGlu 895  
Db 3219 GGGAGCATTTCCCAATCTTAGACATTTTCGATTTTACAAATTTGAGCAGCTAAGAGAT 3278  
QY 895 eArgPheGluAspGlySerSerProLeuLeuGluLysIleGluLysGluCysArgLe 915  
Db 3279 TAGATTGAGGACGCGAGCTCAATCTTTGTTGGAAGATAGAAATATT-CAG---GGGT 3334  
QY 915 uGluSerGlyIleThrGlyIleIleHisLeuProLysLeuLysGluIleProIleArgTy 935

Db 3335 GGAATCAGGAGATTGTTGGTATCATTCCTTCAAGGCTCAAGGAGATTTTCATTGGATA 3394  
QY 935 rGlySerLysValAlaGlyLeuGlnLeuGluGlyGluValAsnAlaHisProAsnAr 955  
Db 3395 CGAAGTAAAGTGGCTAGGCTTGGTCACTGGAGGAGAGAGTGGCAGACACACCAATCA 3454  
QY 955 gProValLeuLeuMetTySerAspArgArgTyrHisAspLeuGlyAlaGluAlaGlu 975  
Db 3455 CCCGATGATGGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3514  
QY 975 ySerSerIleGluValGlnThrAlaAspProValProAspAlaGluGlySerValThrVa 995  
Db 3515 ATCCCTGTTGAA----- 3527  
QY 995 lAlaValAlaAlaThrAspProLeuProGluGlnGluGlyGluSerSerGlnVa 1015  
Db 3528 ---GTGAGAGCAACAGATCTCTG-----GAGAGCTCGAGTTCCAGGT 3567  
QY 1015 lIleThrLeuThrThrAsnAsp----- 1022  
Db 3568 GATCAGCTTGACAAACGAGACAGAGTCACTCCCTACACGGCATCTTAATGAACTTG 3627  
QY 1022 ----- 1022  
Db 3628 TTTTATCTCTGTGAGATCGATGATTTTAACTCACCCTTTCATCTCTCTCTCTCTTA 3687  
QY 1023 -----SerGluGluIleGlyThrAlaGlnAlaGly 1032  
Db 3688 ACCTAACAGCGAGAGATAGACACAACTTAAGCTGT 3724

RESULT 13  
US-10-656-394A-1  
; Sequence 1, Application US/10656394A  
; Publication No. US20040210957A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang et al.  
; TITLE OF INVENTION: Cloning and Characterization of the  
; TITLE OF INVENTION: broad-spectrum resistance gene P12  
; FILE REFERENCE: 035718/252062  
; CURRENT APPLICATION NUMBER: US/10/656,394A  
; CURRENT FILING DATE: 2003-09-05  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 2982  
; TYPE: DNA  
; ORGANISM: Oryza minuta  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(2982)  
US-10-656-394A-1

Alignment Scores:  
Pred. No.: 1.15e-279 Length: 2982  
Score: 3072.00 Matches: 614  
Percent Similarity: 76.5% Conservative: 144  
Best Local Similarity: 62.0% Mismatches: 223  
Query Match: 58.3% Indels: 10  
Gaps: 4

US-10-656-394A-8 (1-1032) x US-10-656-394A-1 (1-2982)

QY 2 AlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAlaAla 21  
Db 7 GCGGAGACCGTGGTGGATGCGGATGCGTCTGGGAGCGCGCTCGGGAAGCGCC 66  
QY 22 SerAlaAlaAspGluThrSerLeuLeuGlyValGluLysAspIleTyIle 41  
Db 67 TCGCGCGCGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 126  
QY 42 LysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysLys 61  
Db 127 AAGGACGAGCTGAAACATTAATTCAGGATCTTAAGAGCTCTTAAGAGTAAACAAGAAGAA 186

Qy 62 AspGluLeuLeuValTrpAlaGluGlnIleArgAspLeuSerTyrAspIleGluLeu 81  
Db 187 GATGACTTCTGAAGGATGGGACAGACAGATCGATCTGTATATACATTAAGAT 246  
Qy 82 SerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuValLys 101  
Db 247 TGCCTAGACGAATTCAGGTTTCATGTTGAGAGCCAAAGCTTGGCAAGCACTAATGAG 306  
Qy 102 LeuArgGluArgHisArgIleAlaIleArgIleHisIleLeuValLysValGluGlu 121  
Db 307 CTTGGTGAACGCCATCGAATTCGTACAGATTCGCAACTTAAATCAAGAAATGAAGAA 366  
Qy 122 ValSerArgAsnThrArgTyrSerLeuValLysProIleSerSer--GlyThrGlu 140  
Db 367 GTGAGCAACAGGANTACAGCTACAGCTTAATCAAGCCCATTTCTCTATACCAACAG 426  
Qy 141 IleAspMetAspSerTyrAlaGluAspIleArgHisGlnSerAlaArgHisValAspGlu 160  
Db 427 GATGAGAGGATTCCTACCTAGAGATGCTCGCAATCGATCAGTAGCAACACTGACGAG 486  
Qy 161 AlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeuGluMetIleAspThrAsn 180  
Db 487 TCGAACTTGTGGGCTTTCGCAAGACTTAAAGATGAGTGTCTTAACCTGATAGATGCAAT 546  
Qy 181 AlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyGlyLeuGlyLysThr 200  
Db 547 ACTAATGACGGTCCAGCTTAAAGTATGATGTGTGGTGTGGTATGGGATAGGCAAGACT 606  
Qy 201 AlaLeuSerArgLysPheSerLeuAspGluSerLeuGluMetIleAspThrAsn 220  
Db 607 ACCCTTGCAGGAGGATATGAAACAGAGNACATG---AAGAACTTCTCGTGTGT 663  
Qy 221 AlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAspMetIleArg 240  
Db 664 GCTTGGATCACTGTGTCTCAGTCACTTTCAGAGGAAAGAAATTCGAAACAAATGATCAGG 723  
Qy 241 GlnLeuLeuGlyProSerSerLeuAspGlnLeuGlnLeuGlnGlyLysValVal 260  
Db 724 CAACCTCTGGGTGTGATTCATAGCAACACTTGAAGAAATTTAGTGAAGATGTGCTC 783  
Qy 261 ValGlnValHisLeuSerGluTyrIleLeuIleGluLeuLeuLysGlyLysArgTyrPhe 280  
Db 784 GTGCAAGTCCAGACTCTCGTGTGATCACTGTGTGTTCAAGGGCTTAAAGGAGAAAGTACTTT 843  
Qy 281 ValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAlaPhe 300  
Db 844 GTTGTCTTGTGATGACCTATGGACCATAGATGATGCAAGAAATTTGATGATATGTCTTT 903  
Qy 301 ProLysAsnAsnLysLysGlySerArgIleValIleThrThrArgAsnValAspLeuAla 320  
Db 904 CCGAAGATTAAACACAGAGGTAGTCGCATAATAATAACACGCGAGATGCTGGCTTAGCT 963  
Qy 321 GluLysCysAlaThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAspAla 340  
Db 964 GGAAGGTGTACCTTGAATCACTATTATTAACACCTTGAACCGTTATCATATGATGATGCT 1023  
Qy 341 IleThrLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsn 360  
Db 1024 ATACACTTGTACTAGCAACAGCAACAAACATAAGACTTGAAGACATGGAATGATGAGGAC 1083  
Qy 361 MetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeu 380  
Db 1084 TTGGGACGATAGTTACAAATTTGGTGAAGGTTGGTGTATTTACCGTGGCTATATCTC 1143  
Qy 381 ThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyrGluHis 400  
Db 1144 ACAATAGGAGGCACTTCTTGTCTACTAAGAGATATGAGTGGGGGAAATTTTACAGAGAA 1203  
Qy 401 LeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgMetValThrLeu 420  
Db 1204 CTTCTCTAGAGCTTTGAGCAATCCAAAGCTTAGAGCCATGAGGAGGATGTGTGACCCCTA 1263

Qy 421 GlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePhePro 440  
Db 1264 AGCTCAATCACTTACCATCTCATCTTAAACCACTGCTTCTTTTACCATAAGTATTTTCCCT 1323  
Qy 441 GluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheVal 460  
Db 1324 GAAGATTTTGAATTCAAAGAGGGGCTGTGTAGATAGATAGATAGACAGAGGTTTGTCT 1383  
Qy 461 ArgProLysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeuIle 480  
Db 1384 AGAGCCACAGATGGGGTGAACATTCAGGATGTGGAAATAGTCACTTTTATGAGCTTATC 1443  
Qy 481 AsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArg 500  
Db 1444 AACAGAGTCTGATTCAGCCCTCAAAAGTTAGTAGAGTGGATGTGTTAAGAGATGTCGA 1503  
Qy 501 IleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGlnAsnPheValLeu 520  
Db 1504 ATCCATGATATCATGCGGTGATATCATAGTTTCAATTTCTAGAGAGGAAATTTTGTGCTG 1563  
Qy 521 LeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHis 540  
Db 1564 TTGACTAGGAGAGATCACTGTTGTAGCGAGAGAGCATCCGCCATCTAGCAATTCAT 1623  
Qy 541 GlySerMetSerCysLysThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIlePhe 560  
Db 1624 GGGAGCAAAATGCTCAAAAGATATGCTTGGAGTGAAGCACTGCGCTCAGTAATTTGTTT 1683  
Qy 561 GlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArg 580  
Db 1684 GCGACACACTGTGGGCGGACACCTGCGACTTTGTTCCACCAATTTAGGATGCTGAGA 1743  
Qy 581 ValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAla 600  
Db 1744 GTGTTGGATCTGGAAGATGCAAAATTCAAATTCACACAAATGATATCAGAAATATAGG 1803  
Qy 601 LeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuPro 620  
Db 1804 TTGTTGCCACATCGAAATTTTGAATTTTGCAGAGGCTCAACTATTTATACATTTCCA 1863  
Qy 621 ArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAla 640  
Db 1864 AGGTCCATAGGAAATTTGCAGTGTTCGCAAAATTTTGAACATGAGGAGGCAATATCTCA 1923  
Qy 641 AlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGln 660  
Db 1924 GCACCTAACACTGAGGTGACTTAACTCCAGATCTCCGATGCTCCGATGCGAGGAGG 1983  
Qy 661 PheHisTyrAspAsnPheSer---LeuAsnHisProMetLysCysIleThrAsnThrIle 679  
Db 1984 TCTGTTCTGTTTACTTTAGCATATAGATAATCCCAAGGAATGCTTGATGATCACCATG 2043  
Qy 680 CysLeuProLysValPheThrProLeuValSerArgAspAspArgAlaLysGlnIleAla 699  
Db 2044 TGTCTTACCGATGGTTTCTTAACCTCAATAAATTTTCAAGTGTGAGTGAATTAATCCT 2103  
Qy 700 GluLeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLys 719  
Db 2104 GAGATATGATGTCATGTCATCTCTCCGCTGTCTGATACAAAGGGTGTGAGGGTGCAGA 2163  
Qy 720 GlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgThrSer 739  
Db 2164 GGAATTTGAACCTTAAAGAGTTACAGATTTCTAGAGTCTGATGATCAACAGAACTAGT 2223  
Qy 740 SerArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrThr 759  
Db 2224 AGGAAGCGGATTTGAAGAGCTGGGGAGCTAAATTCAGTTAAGAAATTAAGCGTGACA 2283  
Qy 760 AsnGlySerThrLysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSer 779  
Db 2284 AAAGCGCCCAAAATAAGAGTATTCAGATATTTTGTGACGAGGATTTGAGAGGCTCTCTCT 2343  
Qy 780 LeuGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLeu 799





LENGTH: 2940  
 TYPE: DNA  
 ORGANISM: Oryza minuta  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (1)..(2940)  
 OTHER INFORMATION:  
 US-10-352-179-84

Alignment Scores:

Pred. No.: 7,19e-279 Length: 2940  
 Score: 3063.50 Matches: 611  
 Percent Similarity: 77.4% Conservative: 141  
 Best Local Similarity: 62.9% Mismatches: 217  
 Query Match: 58.2% Indels: 3  
 DB: 6 Gaps: 3

US-10-656-394A-8 (1-1032) x US-10-352-179-84 (1-2940)

Qy 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerIysAla 20  
 Db 1 ATGGCGGAGACGGTGGTGGATGCGGATGCGGTCGGGCGCGCGCGGAGGCC 60  
 Qy 21 AlaSerAlaAlaAlaAspGluThrSerLeuLeuGlyValGluIysAspIleThr 40  
 Db 61 GCCTCCGCGCGCGCGGAGGAGCCCTCTCTGCTGGGCTCCAGAGGAGATCTGGTAC 120  
 Qy 41 IleIysAspGluLeuLeuThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetIysLys 60  
 Db 121 ATCAAGGACGAGCTGAAACTATTTCAGGCATCTTAAAGCTGCTGAAGTAAACAAGAG 180  
 Qy 61 LysAspGluLeuLeuLysValTrpAlaGluGlnIleArgAspLeuSerTyAspIleGlu 80  
 Db 181 AAAGATGACTTGTAAAGGTATGGCGAGAGCAAGTACGAGATCTGCTATATAACATTGAA 240  
 Qy 81 AspSerLeuAspGluPheLysValHisIleGluSerGlnThrLeuPheArgGlnLeuVal 100  
 Db 241 GATTCCTAGACGAATTCAGGTTCATGTTGAGAGCAAGCTTGGCAACCACTAATG 300  
 Qy 101 LysLeuArgGluArgHisArgIleAlaIleAlaArgIleHisAsnLeuLysSerArgValGlu 120  
 Db 301 AAGCTTGTGTGAACGCCATCGAATGCTGTACAGATCTCAACTTAAATCAAGAATTGAA 360  
 Qy 121 GluValSerSerArgAsnThrArgTySerLeuValLysProIleSerSer---GlyThr 139  
 Db 361 GAAGTGAACAACAGCAATACACGCTACAGCTTAATCAGCTCATTTCTCTATACCAACA 420  
 Qy 140 GluIleAspMetAspSerTyAlaGluAspIleArgAsnGlnSerAlaArgAsnValAsp 159  
 Db 421 GAGGATGAGAGGGATTCCTACCTAGAGATGCTCGCAATCGATCAGGTAGCAACACTGAC 480  
 Qy 160 GluAlaGluLeuValGlyPheSerAspSerLysArgLeuLeuGluMetIleAspThr 179  
 Db 481 GAGTCAGAACTTTGGGCTTTGGCAAGACTTAAAGATGAGTGTCTTAAACTGATAGATGC 540  
 Qy 180 AsnAlaAsnAspGlyProAlaLysValIleCysValValGlyMetGlyLeuGlyLys 199  
 Db 541 AATACTAATGACGCTCCAGCTAAGTGATATGTTGTTGGAATGGGTGGATTAGGCAAG 600  
 Qy 200 ThrAlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCys 219  
 Db 601 ACTACCTTTCAGAGGAGGATATGAAGAAACAGGAAACACATG---AAGAACTTCTCGGT 657  
 Qy 220 AsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLysAspMetIle 239  
 Db 658 TGTGCTGGATCACTGTGCTCAGTCATTTCAGGAGAAAGAAATTCGAAACAATGATC 717  
 Qy 240 ArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuGlnGluGlnGlyVal 259  
 Db 718 AGGCAACTTCTGGGTGCTGATTCATTAGACAAACTCTTGAAGAATTTAGTGAGAGATTG 777  
 Qy 260 ValValGlnValHisIleSerGluTyLeuIleGluLeuLysGluLysArgTy 279

Db 778 CTCGTGCAAGTCCAGCATCTCGCTGATCCTTGGTTGAAGCGCTAAAGAGAAAGGTAC 837  
 Qy 280 PheValValLeuAspAspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAla 299  
 Db 838 TTTGTTGCTCCTTGTGATGACCTTATGGACATAGATGCAATGGAAATGGATTCATGATACGTCT 897  
 Qy 300 PheProLysAsnAsnLysLysGlySerArgIleValIleThrTrpArgAsnValAspLeu 319  
 Db 998 TTTCCGGAAGATTAAACAACAGAGGTAGTCATATATATATATATATATATATATATATATAT 957  
 Qy 320 AlaGluLysCysAlaThrAlaSerLeuValTyHisLeuAspPheLeuGluMetAsnAsp 339  
 Db 958 GCTGGAAGGTGATACCTCTGAATCACTATTATACCACTTGAACCGCTTATCATATATAGATGAT 1017  
 Qy 340 AlaIleThrLeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLys 359  
 Db 1018 GCTATACACTTGTCTACTAGCAAGACAAACATACACTTGAAGACATCGAAGAAATGATGAG 1077  
 Qy 360 AsnMetGlnLysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIle 379  
 Db 1078 GACTTGGGCGAGCATAGTACAAAATTTGGTAAAAAGGTGTGGTTATTTACCGCTGGCTATA 1137  
 Qy 380 LeuThrIleGlyAlaValLeuAlaThrLysGlnValSerGluTrpGluLysPheTyGlu 399  
 Db 1138 CTCACAATAGAGGCACTTCTGCTACTAAGAAAGATAATGGAAATGGGAAATTTTACAGA 1197  
 Qy 400 HisLeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgMetValThr 419  
 Db 1198 GAACCTCTTCAGAGCTTGAGAGCAATCCAGCCCTAGAACCATGAGGAGGATGGTGACC 1257  
 Qy 420 LeuGlyTyAsnHisLeuProSerHisLeuLysProCysPheLeuTyLeuSerIlePhe 439  
 Db 1258 CTAAGCTACCAATCACATTACCTCATCTTAAACCATGCTTTCTTTACCTAAGTATTTC 1317  
 Qy 440 ProGluAspPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPhe 459  
 Db 1318 CCTGAGATTTTCAAAATTCAAAGAGGCGCTTGTAGATAGATAGATGATGAGAGGGTTTT 1377  
 Qy 460 ValArgProLysValGlyMetThrThrLysAspValGlyGluSerTyPheAsnGluLeu 479  
 Db 1378 GTACAGGCCACAGATGGGTGAACATTTAGGAGTGTGGAAATAGTCACTTTAATGAGCTT 1437  
 Qy 480 IleAsnArgSerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCys 499  
 Db 1438 ATCAACAGAGATCTGATTCAGCCCTCAAAAGTTAGTACAGATGGAGTTGTTAAGAGATGT 1497  
 Qy 500 ArgIleHisAspIleIleArgAspIleThrValSerIleSerArgGlnGluAsnPheVal 519  
 Db 1498 CGAATCCATGATATATGCTGATATCATAGTTTCAATTTCTAGAGAGGAAAAATTTGTG 1557  
 Qy 520 LeuLeuProMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPhe 539  
 Db 1558 CTGTTGCTAGGAGAGATCACTGTTGTAGCGGAGGAGAGATCCGCCATCTAGCATTT 1617  
 Qy 540 HisGlySerMetSerCysLysThrGlyLeuAspTrpSerIleIleArgSerLeuAlaIle 559  
 Db 1618 CATGGAGCAAAATGCTCAAAAGATATGCTTGGAGTGGAAACCATCTCGCTCAGTAACCTTG 1677  
 Qy 560 PheGlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeu 579  
 Db 1678 TTTGGTGACAGACTCGCGGGGGAACCTCGACCTTGTTCACCAATTTAGGATGCTG 1737  
 Qy 580 ArgValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIle 599  
 Db 1738 AGAGTGTGATCTGGAAGATGCAAAATTCAAAATTCACAAATATGATATCAGGAATATA 1797  
 Qy 600 AlaLeuLeuCysHisLeuLysTyLeuSerIleGlyTySerSerSerIleTySerLeu 619  
 Db 1798 GGGTGTGTGCGCACATGAATATTTGAATTTTGCAGAGGCTCACTATTATTACACTT 1857  
 Qy 620 ProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyIle 639  
 Db 1858 CCAAGGTCCATAGAAAAATTCAGTGTGCTTGCATAATTTTGAACATGAGGAGGCAATATC 1917



```
Oy 640 AlaAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGly 659
Db 1918 TCAGCACTAACAACTGAGGTGACTTAACTCCAGAACTCTCGTAGCTCCGATGCAGCAGG 1977
Oy 660 GlnPheHisTyrAspAsnPheSer---LeuAsnHisProMetLysCysIleThrAsnThr 678
Db 1978 AGGTCAAGTTCCTGGTTACTTTAGCATATAGATAATCCCAAGAAATGCTTGATATCACC 2037
Oy 679 IleCysLeuProLysValPheThrProLeuValSerArgAspArgAlaIleGlnIle 698
Db 2038 ATGTCTTACCGCATGGTTTCTCAACTTCAATAAATTCAGTGACCGTGTCAAGTTAAT 2097
Oy 699 AlaGluLeuHisMetAlaThrLysSerCysTyrSerGluSerIleGlyValIleValPro 718
Db 2098 CCTGAGATATCATGTATGTTCTACCCGTTGGTCTGTATACAAAGGGTGTGAGGTGCCA 2157
Oy 719 LysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgThr 738
Db 2158 AGAGGAATTTGACAACTTAAAGAGATTACAGATTCTAGAAGTCTGTGCATCAACAGAACT 2217
Oy 739 SerSerArgAlaIleLysLeuGluGlnLeuSerLysLeuArgLysLeuGlyValThr 758
Db 2218 AGTAGAAGGCGATTTGAAGAGCTGGGGAGCTAATTCAGTTAAGAAATTAAGCGTGACA 2277
Oy 759 ThrAsnGlySerThrLysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSer 778
Db 2278 ACMAAGGCGCCACAAATAAGAGTATACAGATATTTGTGCAGCGATTGAGAGCTCTCT 2337
Oy 779 SerLeuGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCys 798
Db 2338 TCTCTGCAATCTCTCCGTGGAGTGTGAGGGATTCTCAGATACCTGGAACACTTGGATGG 2397
Oy 799 LeuAspSerIleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeu 818
Db 2398 CTCAAATTCGATTGCTGCTCTCTCCATTCTTGAAGACACTCAAGTTCGAATGATCTCTT 2457
Oy 819 GluGluMetProAsnThrIleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeuArg 838
Db 2458 GCAGATACACCAAACTGGTTGGGAACCTTTAAGCAGCTGTGTGAAGATGTGCTTATCCAGA 2517
Oy 839 SerLysLeuLysGluGlyLysThrMetLeuIleLeuGlyValAlaLeuProAsnLeuMetVal 858
Db 2518 TGTGTGCTTACAAGATGTGTAATACTATGGAGATACTTTGGGGCACTGCCCACTTATGTT 2577
Oy 859 LeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLysLeuValPheLysThrGlyAlaPhe 878
Db 2578 CTTGCTCTTTATCGCAACGCATATGCTGCAGAGAAATGGCAATTCAGAAAGGGGAACATC 2637
Oy 879 ProAsnLeuArgThrLeuThrIleTyrGluLeuAspGlnLeuArgGluIleArgPheGlu 898
Db 2638 CCAAACTCTCAGGTGCTCTTGATATTTACTTGTCTGAAGCACTTTAGAGAGATAAGATTGAG 2697
Oy 899 AspGlySerSerProLeuLeuGluLysIleGluIleGlyGluCysArgLeuGluSerGly 918
Db 2698 GAGGCACTCTGCCCAACATGGAAAGTATAGAAATTTATGGTTCCAGGTTGGAATCAGGG 2757
Oy 919 IleThrGlyIleIleHisProLysLeuLysGluIleProIleArgTyrGlySerLys 938
Db 2758 AFTATTGGTATCAAGCACTTCCAGACTTTAGATTATTTCCGTTGAATATATGTTGTTAA 2817
Oy 939 ValAlaGlyLeuGlyGlnLeuGluGlyGluValAsnAlaHisProAsnArgProValLeu 958
Db 2818 CTCGCGAAGCTTGATGTGTCGAAGAGGAAGTGAATACACACCCCAATCATCTACTGAACTG 2877
Oy 959 LeuMetTyrSerArgArgTyrHisAspLeuGly 970
Db 2878 CAATGGCAGAGGATCGAAGTCATCATGACCTAGGA 2913
```

Search completed: March 9, 2006, 23:23:39  
Job time : 1957 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 9, 2006, 22:52:26 ; Search time 2260 Seconds  
(without alignments)  
1053.598 Million cell updates/sec

Title: US-10-656-394A-8

Perfect score: 5268

Sequence: 1 MAEVLMSRLVGSALSKA.....SQVITLTNDSEIGTAQAG 1032

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 7673375 seqs, 1153648444 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp  
-O=/abs/ABSSWEB.spool/US10656394/runat.09032006.094027.822/app.query.fasta.1  
-DB=Published Applications NA New -QWTF=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
-MAXLEN=200000000 -HOST=absos3p  
-USER=US10656394 @CGN 1 1 653 @runat.09032006.094027.822 -NCPU=6 -ICPU=3  
-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:  
1: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	668.5	12.7	2151	9 US-11-031-206-125	Sequence 125, App
2	541.5	10.3	1861	9 US-11-031-206-115	Sequence 115, App
3	524	9.9	1944	9 US-11-031-206-109	Sequence 109, App
4	474	9.0	1902	9 US-11-031-206-137	Sequence 137, App

5	357.5	6.8	813	9 US-11-031-206-127	Sequence 127, App
6	322.5	6.1	4671	9 US-11-096-568A-30746	Sequence 30746, A
7	309	5.9	2382	9 US-11-031-206-101	Sequence 101, App
8	298	5.7	644	9 US-11-031-206-107	Sequence 107, App
9	250	4.7	4585	9 US-11-096-568A-34295	Sequence 34295, A
10	237.5	4.5	629	9 US-11-031-206-133	Sequence 133, App
11	225	4.3	634	9 US-11-031-206-139	Sequence 139, App
12	206.5	3.9	1892	9 US-11-031-206-105	Sequence 105, App
13	203.5	3.9	785	9 US-11-031-206-121	Sequence 121, App
14	187	3.5	306	9 US-11-031-206-133	Sequence 133, App
15	186.5	3.5	549	9 US-11-031-206-119	Sequence 119, App
16	183	3.5	6773	8 US-10-947-249-105	Sequence 105, App
17	169	3.2	3725	9 US-11-096-568A-32720	Sequence 32720, A
18	168.5	3.2	585	9 US-11-031-206-113	Sequence 113, App
19	167.5	3.2	3647	7 US-11-096-568A-31266	Sequence 31266, A
20	163	3.1	5658	7 US-10-932-182A-6026	Sequence 6026, App
21	163	3.1	5658	7 US-10-932-182A-6026	Sequence 6026, App
22	162	3.1	1257	9 US-11-096-568A-29993	Sequence 29993, A
23	161	3.1	10211	12 US-11-000-688-98	Sequence 98, App
24	160	3.0	2943	9 US-11-010-239-126	Sequence 126, App
25	159.5	3.0	2966	9 US-11-072-512-157	Sequence 157, App
26	156.5	3.0	3117	7 US-10-932-182A-2299	Sequence 2299, App
27	156.5	3.0	3117	7 US-10-932-182A-2299	Sequence 2299, App
28	154.5	2.9	3008	12 US-11-010-239-114	Sequence 114, App
29	154.5	2.9	3309	9 US-11-096-568A-27956	Sequence 27956, A
30	154	2.9	17642	8 US-10-995-561-256	Sequence 256, App
31	153	2.9	16792	8 US-10-995-561-262	Sequence 262, App
32	153	2.9	17292	8 US-10-995-561-260	Sequence 260, App
33	153	2.9	17436	8 US-10-995-561-257	Sequence 257, App
34	153	2.9	17507	8 US-10-995-561-254	Sequence 254, App
35	153	2.9	17610	8 US-10-995-561-258	Sequence 258, App
36	153	2.9	19023	8 US-10-995-561-259	Sequence 259, App
37	151.5	2.9	10300	8 US-10-947-249-122	Sequence 122, App
38	150.5	2.9	3251	9 US-11-096-568A-34461	Sequence 34461, A
39	150.5	2.9	5127	12 US-11-136-527-3255	Sequence 3255, A
40	149.5	2.8	14121	9 US-11-200-710-1	Sequence 1, Appli
41	149.5	2.8	14121	12 US-11-124-020A-10	Sequence 3, Appli
42	149.5	2.8	14121	12 US-11-123-656A-3	Sequence 135, App
43	148.5	2.8	550	9 US-11-031-206-135	Sequence 349, App
44	148.5	2.8	2479	7 US-10-973-115B-349	Sequence 349, App
45	148.5	2.8	2479	8 US-10-131-826A-349	Sequence 349, App

#### ALIGNMENTS

#### RESULT 1

US-11-031-206-125  
; Sequence 125, Application US/11031206  
; Publication No. US20060031959A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Odell, Joan T.  
; APPLICANT: Meyers, Blake  
; APPLICANT: Thorpe, Catherine  
; APPLICANT: Weng, Zude  
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
; TITLE OF INVENTION: Stress Response  
; FILE REFERENCE: B1357 US NA  
; CURRENT APPLICATION NUMBER: US/11/031,206  
; PRIOR FILING DATE: 2005-01-07  
; PRIOR APPLICATION NUMBER: US/09/566,394  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/133038  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133042  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133427  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133437

; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133428  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133438  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133436  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/137667  
 ; PRIOR FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 208  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 125  
 ; LENGTH: 2151  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; US-11-031-206-125

## Alignment Scores:

Pred. No.: 4.41e-58 Length: 2151  
 Score: 668.50 Matches: 167  
 Percent Similarity: 52.8% Conservative: 103  
 Best Local Similarity: 32.7% Mismatches: 172  
 Query Match: 12.7% Indels: 69  
 DB: 9 Gaps: 16

US-10-656-394A-8 (1-1032) x US-11-031-206-125 (1-2151)

QY 1 MetAlaGluThrValLeuSerMetAlaArgSerLeuValGlySerAlaIleSerLysAla 20  
 DB 702 ATGGCGGAATGGCGAGTCTTCGCACGA-----GACAAATTG 740  
 QY 21 AlaSerAlaAlaAlaAspGluThrSerLeuLeuGlyValGluLysAspIleTrpTyr 40  
 DB 741 CTTCCACTACTAAGCGACGACGAAACCTCTTTGGAACATCCCAAGAAATTGAAGAC 800  
 QY 41 IleLysAspGluLeuLysThrMetGlnAlaPheLeuArgAlaAlaGluLeuMetLysLys 60  
 DB 801 ATCAAAATGAAGTATGATATCAATTCAGGCTCCCTGGAGAGCGAGTAGATGGCTGCA 860  
 QY 61 LysAsp-----GluLeuLeuLysValTrpAlaGluGlnIleArgAspLeu 75  
 DB 861 GAAGAGGAGGACAAACGCAAGGGAATCAAAAAATGGTGAAGGACTTCGAGGGAAGCA 920  
 QY 76 SerTyrAspIleGluAspSerLeuAspGluPheLysValHisIleGluSerGln----- 93  
 DB 921 TCTTTCCGAATGAGAGTGTGATGACACATATCTATGTGTGGAACACCGCTCAT 980  
 QY 94 -----ThrLeuPheArgGlnLeuValLys 101  
 DB 981 GATGCTCTTGGTGTGCGAGCTTTACTCTTTGAGTGAATATCACTCACTTCATTGAATCT 1040  
 QY 102 LeuArgGluArgHisArgIleAlaIleArgIleHisLeuLysSerArgValGluGlu 121  
 DB 1041 TTGAGCGCTGTGTCATCAAAATAGCATCAGAGTTCACAGCATTAAGTCATTGTTTCACGGA 1100  
 QY 122 ValSerSerArgAsnThrArgTyrSer---LeuValLysProIleSerSerGlyThrGlu 140  
 DB 1101 ATCAAGCAAGAGGATTTGATTATGACTACCTAATCAACCT-----TCTCTTGAG 1151  
 QY 141 IleAspMetAspSerTyr-----AlaGluAspIleArg-----AsnGlnSer 154  
 DB 1152 CACGGATCAGCAGCTCAGAGGAGGCAAAAGTGTCCAATGGCATGACCCCTGATTGGCT 1211  
 QY 155 AlaArgAsnValAspGluAlaGluLeuValGlyPheSerAspSerLysLysArgLeuLeu 174  
 DB 1212 TCACGCTTACCTTGCAGAGCGGAAGTGTGGCTTTGAAGACCCCTAAAGAGTAATGATA 1271  
 QY 175 GluMetIleAspThrAsnAlaAsnAspGlyProAlaLys-----ValIleCysVal 192  
 DB 1272 -----ACTGTGTAGTGAAGGACCGAGGAGCGACCATCATCTTTGTGTA 1319  
 QY 193 GlyMetGlyLeuGlyLysThrAlaLeuSerArgLysIlePheGluSerGluGluAsp 212

DB 1320 GGAATGGAGGGCTAGGAAAAACAACATGTTGCGGAGAGTCTTCAATAACAGAGAGTG 1379  
 QY 213 IleArgLysAsnPheProCysAsnAlaIleTrpIleThrValSerGlnSerPheHisArgIle 232  
 DB 1380 ATT---GCACACTTTGATTGCTCCATGATGCATCACAGTGTCTCAATCTCACAATGTGAA 1436  
 QY 233 GluLeuLeuLysAspMetIleArgGlnLeuLeuGlyProSerSerLeuAspGlnLeuLeu 252  
 DB 1437 GGGTGTCTAAGAGACTTTGTAAGAAGTTATGCAAGAAAGAGAGTGTGTTGTTGTTGAT 1487  
 QY 253 GlnGluLeuGlnGlyLysValValGlnValHisHisLeuSerGluTyr----- 269  
 DB 1488 -----CCTCCTCATGATATTCTTGAATGAATCAATCGAGAT 1520  
 QY 270 ---LeuIleGluGlu-----LeuLysGluLysArgTyrPheValValLeuAsp 284  
 DB 1521 TCACCTGATTGATGAGTGAAGACCCATTTGGGAGTCAAAATGAAATGCGATGCTT--- 1580  
 QY 285 AspLeuTrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAlaPheProLysAsnAsn 304  
 DB 1581 GATGTATGGAGTGTAGAACCTTTGGGAGTCAAAATGAAATGCGATGCTT---GATACT 1634  
 QY 305 LysLysGlySerArgIleValIleThrThrArgAsnValAspLeuAlaGluLysCysAla 324  
 DB 1635 AAAAAATGGTGTAGAATATTATATCACTAGGATGGATGGTGTGTAGACTCTTTGATG 1694  
 QY 325 -----ThrAlaSerLeuValTyrHisLeuAspPheLeuGlnMetAsnAlaIleThr 342  
 DB 1695 AAATATCTTCGGATGAGTGCATAGCTGAAACCTTTGACTCAAGAAGATCTATGCAA 1754  
 QY 343 LeuLeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsnMetGln 362  
 DB -1755 CTTCTTTGCAAGAGGACATACCGATACCAATAATGGGCATTTGCCAGAAGATCTTAAG 1814  
 QY 363 LysMetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeuThrIle 382  
 DB 1815 AAAATTTCTTCTGACTTTGTTGAAAAATGTAAGGTTTACCATTGGCAATTTGGCTATT 1874  
 QY 383 GlyAlaValLeuAlaThrLysGlnValSer-----GluTrpGluLysPheTyrGluHis 400  
 DB 1875 GGTAGTCTTTTCTGCGCAAGAAAGACTCCATTGTAATGGGAAAAAATTTAGCGAAGC 1934  
 QY 401 LeuProSerGluLeuGluIleAsnProSerLeuGluAlaLeuArgArgMetValThrLeu 420  
 DB 1935 CTAAGTTTCAGAGATGAACAAAGTCCCACTTTAATGGCATAACAAGATTTTAGTTTC 1994  
 QY 421 GlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeuSerIlePhePro 440  
 DB 1995 AGTTATGATGATTGGCATATTATCTGAAATCATGCTTTATTGTTTGGTGTATATCCC 2054  
 QY 441 GluAspPheGluIleLysArgAsnArgLeuValGlyArgTyrIleAlaGluGlyPheVal 460  
 DB 2055 GAAGCTATGAGTGAATCAAAAGATTAATTTGGCAATGGATAGCTGAAGGATTGTA 2114  
 QY 461 ArgProLysValGlyMetThrLysAspVal 471  
 DB 2115 AAAGAGGAAGAGGAAAAACATTAGAGGACCTC 2147

## RESULT 2

; US-11-031-206-115  
 ; Sequence 115, Application US/11031206  
 ; Publication No. US20060031959A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rafalski, Antoni  
 ; APPLICANT: Miao, Guo-Hua  
 ; APPLICANT: Falco, Saverio Carl  
 ; APPLICANT: Sakai, Hajime  
 ; APPLICANT: Famodu, Omolayo O.  
 ; APPLICANT: Odell, Joan T.  
 ; APPLICANT: Meyers, Blake  
 ; APPLICANT: Thorpe, Catherine  
 ; APPLICANT: Weng, Zude  
 ; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in

TITLE OF INVENTION: Stress Response  
FILE REFERENCE: BB1357 US NA  
CURRENT APPLICATION NUMBER: US/11/031.206  
CURRENT FILING DATE: 2005-01-07

PRIOR APPLICATION NUMBER: US/09/566.394  
PRIOR FILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: 60/133038  
PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133042  
PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: 60/133427  
PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133437  
PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133428  
PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133438  
PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/133436  
PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 60/137667  
PRIOR FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 208

SOFTWARE: Microsoft Office 97

SEQ ID NO 115

LENGTH: 1861

TYPE: DNA

ORGANISM: Oryza sativa

US-11-031-206-115

Alignment Scores:  
Pred. No.: 4.56e-45 Length: 1861  
Score: 541.50 Matches: 171  
Percent Similarity: 46.2% Conservative: 107  
Best Local Similarity: 28.4% Mismatches: 233  
Query Match: 10.3% Indels: 91  
DB: 9 Gaps: 19

US-10-656-394A-8 (1-1032) x US-11-031-206-115 (1-1861)

QY 346 ArgLysThrAsnLysAsnHisGluAspMetGluSerAsnMetGlnLysMetVal 365  
DB 17 AGAAGGGCAATTTTAAACATTAAGGACCATGAGTGTCCCGAAGTGGCC 76  
QY 366 GluArgLysValAsnLysCysGlyArgLeuProLeuAlaLeuThrLeuGlyAlaVal 385  
DB 77 AAATCTATAGTTGAGGGGTGTGAGGGCTTCCACTAGCAATTTGTCAATAGGCTGCTC 136  
QY 386 LeuAlaThrLysGlnValSerGlu-----TrpGluLysPheTyrGluHisLeuProSer 403  
DB 137 CTGCTTCAAGATCAGGTCACATATATGTTTGGAAATCAGCATACATCACTAGAACT 196  
QY 404 GluLeuGluAlaAsnProSerLeuGluAlaLeuArgMetValThrLeuGlyTyrAsn 423  
DB 197 GAGTGTCTCAAGAAC-----AATCATGTCCGAGCAATTTTAAATATGAGCTACCAT 247  
QY 424 HisLeuProSerHisLysLysProCysPheLeuTyrLeuSerLeuPheProGluAspPhe 443  
DB 248 GACCTGTGAGGAGACCTAAGAACTGCTTTTGTACTGAGGCTTATTCGCGAAGACTAC 307  
QY 444 GluLysLeuArgAsnArgLeuValGlyArgTrpLeuAlaGluGlyPheValArgProLys 463  
DB 308 CCCTCTCCGCTGAGAGCCCTGTGCTGTGGATTGCAAGGCTTTGTCTGAGGAA 367  
QY 464 ValGlyMetThrThrLysAspValGlyLysSerTyrPheAsnGluLeuLeuAsnArgSer 483  
DB 368 GAGAACACACACAGGAGCAGTACCTGAGGAAATCTCATGGAATTTGATATACAGAAAT 427  
QY 484 MetIleGluArgSerArgValGlyLysLeuAlaGlyLysLysThrCysArgLysHisAsp 503  
DB 428 ATGCTTCAAGTTACAGAGTATGATGATCTCCGCGAGGTGAATCTTGTGGAATGATGAC 487  
QY 504 IleLeuArgAspIleThrValSerLysSerArgGlnGluAsnPheValLeuLeuProMet 523

DB 488 ATTATGCGAGACCTGGCCCTTCTGCTGCTAAAGAGGAGAAGTTT----- 532  
QY 524 GlyAspGlySerAspLeuValGlnGluAsnThrArgHisLeuAlaPheHisGlySerMet 543  
DB 533 GGTCTGCAATGATTT-----GGCACAATG 559  
QY 544 SerCysLysThrGlyLeuAspTrpSerIleLeuArgSerLeuAlaLeuPheGlyAspArg 563  
DB 560 -----GTAGAGATTGAT---AAGGATGTTGCGTCTGCTCAACTACCGATGGAAA 607  
QY 564 ProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArgValLeuAsp 583  
DB 608 GACAGTACT-----GCACCAATCTCAAACTTCTACGCTTCGACCACTAGTATCA 658  
QY 584 LeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAlaLeuLeuCys 603  
DB 659 CTTGAAGCATTTTTCATCTTCATTTGATGTTGCTCC-----TCAGTTTGTCT 706  
QY 604 HisLeuLysTyrLeuSerIle-----GlyTyrSerSerSerIleTyrSerLeuProArg 621  
DB 707 CACTCAAGCTTACTTACTGTTCTCGAGTTCAGATTCAGAAATCACTCAAGTCCACCA 766  
QY 622 SerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAla 641  
DB 767 TCTATAGGGAATTTGTTTAACTTACGTTTACATTTGCTTACGGAGGACCAAGGTTAAGTCA 826  
QY 642 LeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPhe 661  
DB 827 CTCCGAGACTCCATTTGAAGTTGCTGAACTTCCACTCTG----- 868  
QY 662 HistyrAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCysLeu 681  
DB 869 -----GACATGAAG---CAAACAAGATAGAGAAGTCA 898  
QY 682 ProLysValPheThrProLeuValSerArgAspAspArgAlaLysGlnIleAlaGluLeu 701  
DB 899 CCACGAGGAATCACT-----AAATCAAGAAGCTAAGA----- 931  
QY 702 HisMetAlaThrLysSerCysTrpSerGluSer-----IleGly 714  
DB 932 CACTTGTGTTGCTGATAGATGTTGACGAGACGAGTTCGGAGTTCGGATCTTGTAGGA 991  
QY 715 ValLysValProLysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAsp 734  
DB 992 ATGCGAGCACCTAAAGATCTATCCAACTGAAAGAACTACAACCTCGAGACTGTTGAA 1051  
QY 735 IleArgArgThrSerSerArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLys 754  
DB 1052 GCCAGCAAGGACTTAGCTGAGCAGTTCGAGAACTCATACAACTAAA----- 1099  
QY 755 LeuGlyValThrThrAsnGlySerThrLysGluLysCysLysIleLeuTyrAlaLalle 774  
DB 1100 ---AGTGTATGGATGACACATAGCTCTGCTGATTGTGATTAATATTTTCTACACG 1156  
QY 775 GluLysLeuSerSerLeuGlnSerLeuHisValAspAlaGlyLysSerAspGlyGly 794  
DB 1157 TCAATATGCCGCTACTTCCAGTTTCTTCTTCTGCAAGGAATGAGAATGAGCACTT 1216  
QY 795 ThrLeuGluCysLeuAspSerIleSerSerProProLeuLeuArgThrLeuValLeu 814  
DB 1217 TCTTTTGGGCTCTCAAGCCCAAGTTCACAGAA-----CTCACAGGTTAATGTC 1267  
QY 815 AspGly-----IleLeuGluGluMetProAsnTrpIleGluGlnLeuThrHis 830  
DB 1268 AGAGGGCAATGGCCAGAGTACATTGGACTACCCGATATCCATAGCCACAGTACACAT 1327  
QY 831 LeuLysLysIleTyrLeuLeuArgSerLysLeuLysGluGlyLysThrMetLeuLeu 850  
DB 1328 CTCAAATATTTATCCCTAAGTTGTGTCTCTCGGGAAGATCATTTGGGAGTCTGG 1387  
QY 851 GlyAlaLeuProAsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLys 870

Db 1388 TCAGACTGTGGACCTCTACTTATCTAAACCTG---AACCACTGCAGAGTGCAGCAACA 1444  
 Qy 871 LeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyGluLeuAsp 890  
 Db 1445 TTAGTTCTTCGTGCAAGGCAATCCCAAACTAAAGACTCTTGTCTTGAGGCAGATGCT 1504  
 Qy 891 GlnLeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGluLysIleGluIle 910  
 Db 1505 GATGTCAAGCAGATAAGATCATGTGATGCGCCCTTCATCCATTAAGTGTGTTGATAC--- 1561  
 Qy 911 GlyGluCysArgLeuGluSerGlyIleThrGlyIleIleHisLeuProLysLeuValGlu 930  
 Db 1562 -----ATTGTTGTCTGCGAGCTGGACAG 1588

Qy 931 IlePro 932

Db 1589 GTCCCT 1594

# RESULT 3

US-11-031-206-109  
 ; Sequence 109, Application US/11031206  
 ; Publication No. US2006003195A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rafalski, Antoni  
 ; APPLICANT: Miao, Guo-Hua  
 ; APPLICANT: Falco, Saverio Carl  
 ; APPLICANT: Sakai, Hajime  
 ; APPLICANT: Farnodu, Omolayo O.  
 ; APPLICANT: Odell, Joan T.  
 ; APPLICANT: Meyers, Blake  
 ; APPLICANT: Thorpe, Catherine  
 ; APPLICANT: Weng, Zude  
 ; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
 ; FILE REFERENCE: BB1357 US NA  
 ; CURRENT APPLICATION NUMBER: US/11/031,206  
 ; CURRENT FILING DATE: 2005-01-07  
 ; PRIOR APPLICATION NUMBER: US/09/566,394  
 ; PRIOR FILING DATE: 2000-05-05  
 ; PRIOR APPLICATION NUMBER: 60/133038  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133042  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133427  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133437  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133428  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133438  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133436  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/137667  
 ; PRIOR FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 208  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 109  
 ; LENGTH: 1944  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; US-11-031-206-109

Alignment Scores:  
 Pred. No.: 3,09e-43 Length: 1944  
 Score: 524.00 Matches: 162  
 Percent Similarity: 46.8% Conservative: 107  
 Best Local Similarity: 28.2% Mismatches: 218  
 Query Match: 9.9% Indels: 88  
 DB: 9 Gaps: 19

US-10-656-394A-8 (1-1032) x US-11-031-206-109 (1-1944)

Qy 375 LeuProLeuAlaIleLeuThrIleGlyAlaValLeuAlaThrIle---GlnValSerGlu 393  
 Db 14 CTGCCACTAGCAATTTGTACAGTCGGCAGCTGCTGTCATCTAGACCACAAATAAATTT 73  
 Qy 394 TrpGluLysPheTyGluHisLeuProSerGluLeuGluIleAsnProSerLeuGluAla 413  
 Db 74 TCGAATCAACATCAACACAGCTTCGGAGTGAGTTGTCAACCAAT-----GATCAT 124  
 Qy 414 LeuArgArgMetValThrLeuGlyTyAsnHisLeuProSerHisLeuLysProCysPhe 433  
 Db 125 GTCCGAGCAATCTTAATCTAAGCTACCATGATCTATCTCGAGATCTCAGAAACTGCTTC 184  
 Qy 434 LeuTyLeuSerIlePheProGluAspPheGluIleLysArgAsnArgLeuValGlyArg 453  
 Db 185 TTGTATTCAGCTTGTTCCTGAAGACTACCCATGTCACGCAAGCCCTTTGGGGCTC 244  
 Qy 454 TrpIleAlaGluGlyPheValArgProLysValGlyMetThrThrLysAspValGlyGlu 473  
 Db 245 TGGGTGCGAAGAGTTTGTCTGAGTAAAGAAAGAAATACACAGAGGAGGTGGCTGAG 304  
 Qy 474 SerTyPheAsnGluLeuIleAsnArgSerMetIleGlnArgSerArgValGlyIleAla 493  
 Db 305 GGAATCTCATGGAATGATCCCGTAAATATGCTTGAAGTTGATAGTATGATGAGCTT 364  
 Qy 494 GlyLysIleLysThrCysArgIleHisAspIleIleArgAspIleThrValSerIleSer 513  
 Db 365 GGCAGGGTTAGCACTTGCAGATGATCATGAGGACCTGCGCACTTTGTGTGTC 424  
 Qy 514 ArgGlnGluAsnPheValLeuProMetGlyAspGlySerAspLeu-----529  
 Db 425 AAAGAAGAGAGAGTTT-----GGTTCTGCAACAGATTTATGGTGAAGTATA 469  
 Qy 530 ---ValGlnGluAsnThrArgHisIleAlaPheHisGly---SerMetSerCysLysThr 547  
 Db 470 CAGGTGGACACAGAGTTGCTGCTTGTATGTTGGTGAATTTAAGGACAGCAGCT 529  
 Qy 548 GlyLeuAspTrpSerIleIleArgSerLeuAlaIlePheGly-----561  
 Db 530 AAGTTTAAATTTCCATGCTCCGACTCTTGTGGCTCAGGGAATATTTTCATCTCTCT 589  
 Qy 562 AspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArgVal 581  
 Db 590 GACATGGTATCCTCAATTATG-----TCTCAATCAATTTATTTGACAGTT 634  
 Qy 582 LeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAlaLeu 601  
 Db 635 CTTGAGCTGCAAGATTTCTGAG-----ATCAGTGGAGTGGCCA---GCATTTATAGAAAT 685  
 Qy 602 LeuCysHisLeuLysTyLeuSerIleGlyTySerSerSerIleTySerLeuProArg 621  
 Db 686 CTCCTTAACCTACGGTATATTGGGTTA---AGCGCACCAAGTCAAGTCACTCCACAG 742  
 Qy 622 SerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyIleAlaAla 641  
 Db 743 TCTATTGAGAAGCTCTCAACCTCCACACTCTCGATATCAAAACAACTCAATAGAGAAA 802  
 Qy 642 LeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPhe 661  
 Db 803 CTACCCAGCGGATTTAGTCAAGAGCTTAAGCAGCCTTTTACCT-----850  
 Qy 662 HisTyAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCysLeu 681  
 Db 851 -----GACAGGTTTGTCT-----862  
 Qy 682 ProLysValPheThrProLeuValSerArgAspAlaLysGlnIleAlaGluLeu 701  
 Db 863 -----GATGAGACGACGAGGTTTCAGATATTTC 892  
 Qy 702 HisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLysGlyIle 721  
 Db 893 -----ATCGAGTGGAGAGCCTTAAGGCTG 919  
 Qy 722 GlyLysLeuArgAspLeuGlnValLeuGluTyValAspIleArgArgThrSerArg 741





QY	597	AspargilealaLeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSerSerIle	616
DY	598	:::::	
DB	695	GAAAGACATCTCTG----	742
QY	617	TyrSerLeuProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSer	636
DB	743	ACTGAGCTTCCAAATAACAATTGGAGATTGGGGTTCTTAGAAAACACTTGATGCATCATTT	802
QY	637	ThrTyrllealalaLeuProSerGIulllleSerLysLeuGlnCysLeuHisThrLeuArg	656
DB	803	ACCGAATTGTGTGAGATGCCGTGGATCCATTACTGTCTTAAGAAGACTGAACGCCCTG---	859
QY	657	CysIleGlyGlnPheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIleThr	676
DB	859	-----	859
QY	677	AsnThrIleCysLeuProLysValPheThrProLeuValSerArgAspAspArgAlaLys	696
DB	860	-----TTTGTTCAGTAA-----	874
QY	697	GlnlealagluLeuHisMetalathrLysSerCysTrpSerGluseriIleglyVallys	716
DB	875	-----ACTAAA880-----	880
QY	717	ValProLysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArg	736
DB	881	TTGCTGATGATGGAAACATNG---TGC TTGC AAGAGACTTGGGGATATAAATGCCTTC	937
QY	737	ArgThrSerSerArgAlalleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGly	756
DB	938	AACCAATCAGTTAACTTCTCGAATGAGCTTGGCAAACTAATGAGTCTGCGTAAGCTGAGC	997
QY	757	Val-----ThrThrAsngly-----SerThrLysGluLys---	766
DB	998	ATTATCTGGGACCAACGGTATCCCAGATTGGCAAAAGNAGTTATAGGAANAANAAG	1057
QY	767	-----CysLysIleLeuTyrAlaalleGluLysLeuSerSerLeuGln	781
DB	1058	TTTGTCCTCGCTCTGTAACACTGGATCAGATGGGCGCTTCGCACCCTCTGTGTACATTT	1117
QY	782	SerLeuHisValAspAlaaleGlylleSerAspGlyGlyThrLeuGluCysLeuAspSer	801
DB	1118	TATTTGAGA---GAAAAGGATGGCTTCATTGGNCATCCGTTCTTGCGCTCTCTCAATAGT	1174
QY	802	IleSerSerProProLeuLeuArgThrLeuValLeuAspGlylleLeuGluGluMet	821
DB	1175	ATCCGA-----GAGGTCTATCTCCGCGTGGCGCATGTGTGGATT	1216
QY	822	ProAntTpIleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeuArgSerLysLeu	841
DB	1217	AACAANATGGCTCTTCACTTGCACCACTAGAAAATTTATATATCAGTGGTGGGATGAG	1276
QY	842	LysGluGlyLysThrMetLeulleLeuGlyAlaLeuProAsnLeuMetValLeuHisLeu	861
DB	1277	ATAGACAGGATGATCGCGTACAGTTGGAAGCATACCAACTCTGGTTGAATCAACGCTT	1336
QY	862	TyrgaenalatyrLeuGlyGluLysLeuValPheLysThrGlyAlaPheProAsnLeu	881
DB	1337	TAC--TCTGGATCTTTAGGCGCTATCATCAT-AGTTCAGGATTTTGAACAGTTA	1387
QY	882	ArgThrLeuTpIleTyrGluLeuAsp---GlnLeuArgGluilleArgPheGluAspGly	900
DB	1388	GAGAGGCTC-----GAGTTGAAGTTCAGTTTTTGCAGCTGACGCTTTGAAGTGGCG	1438
QY	901	SerSerProLeuLeuGluLysIleGluilleGlyGluCysArgLeuGluSerGlylleThr	920
DB	1439	GCTATGCCCTAACCTGAAGAAACTTGATCTCCAT-----	1471
QY	921	GlylleleHisLeuProLysLeuLysGluille-----ProIleArg	934
DB	1472	-----GPTTATTATCTAAGTTCAAATCTGTTGGTGGTGGTTTGTATTTGGCATCCAG	1525
QY	935	TyrGlySerLysValalaglyLeu-----	942

```

Db      1586 CATCTCTCCAGCCTTGCTGGTGTCTATCGTCATATATTTCCGAGGGGTCAGTCTGCC 1588
      ::: ||| ::::||| ::::
Qy      943 -----GlycInLeuGluGlyGluValAenAlaHis-----ProAgn 954
      ::::
Db      1586 TATGTGGAGGACGCGGAGGAGGCTTTCAAGAGCATGTGTCAATGGACACACCGAACCCCAAC 1645
      ::::
Qy      955 ArgProValLeuLeuMet 960
      |||:::|||||
Db      1646 CGACCCATATGGGAATG 1663

RESULT 5
US-11-031-206-127
; Sequence 127, Application US/11031206
; Publication No. US20060031959A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odeil, Joan I.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; FILE REFERENCE: BB1357 US NA
; CURRENT APPLICATION NUMBER: US/11/031,206
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: US/09/566,394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 127
; LENGTH: 813
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (813)
US-11-031-206-127

Alignment Scores:
Pred. No.: 1.38e-26 Length: 813
Score: 357.50 Matches: 98
Percent Similarity: 53.4% Conservative: 57
Best Local Similarity: 33.8% Mismatches: 108
Query Match: 6.8% Indels: 27
DB: 9 Gaps: 10

US-10-656-394A-8 (1-1032) X US-11-031-206-127 (1-813)

Qy      156 ArgAsnValAspGluAlaGluLeuValGlyPhe----SerAspSerLysLysArgLeuLeu 174
      |||:::|||||:::
Db      10 AGCGAGGTGGAGGAAGAATGTGTGGCTTAGTGCAATGACTCAAGCCATGTGAATTTCAG 69
      |||:::|||||:::

```



Db 1804 AAATCTTTAGACGAAGAAAGAAAGATATTCCTCGACATTCGATCTCTCTTCTCAAA 1863  
Qy 443 PheGluLeuLysArgAsnArgLeuValGlyArgTTPilleaGluGlyPheValArgPro 462  
Db 1864 ATGGATATACAAAGAAAGAGTGTGCGAC-----ATACGTGAAGGA----- 1905  
Qy 463 LysValGlyMetThrThrLysAspValGlyGluSerTyrPheAsnGluLeuLeuAsnArg 482  
Db 1906 ---TGTTGGGTAAACGCC-----GAGGCTGTCTCCGT 1935  
Qy 483 SerMetIleGlnArgSerArgValGlyIleAlaGlyLysIleLysThrCysArgIleHis 502  
Db 1936 GTTCTTATACAGAAATCTCTCTTACATCTTGACAGAC---GACACTCTGTGCGATCAT 1992  
Qy 503 AspIleLeuArgAspIleThrValSerIleSerArgGlnGluAsn-PheValLeuLeuPr 522  
Db 1993 GATCAGATCAGACATCGGTAGGAGATGTTTCATAAAGAAAGACGCGATGATCTCTGAG 2052  
Qy 522 oMetGlyAspGlySerAspLeuValGlnGluAsnThrArgHisIleAlaPheHisGlySe 542  
Db 2053 ATGCGGAGTAGACTCTGGGATCGTG----- 2077  
Qy 542 rMetSerCysLeuThrGlyLeuAspTrpSerIleLeuArgSerLeuAlaIlePheGlyAs 562  
Db 2078 -----GTGAATAATGAACGTATTGGACTATATGAAGGGAACATCATCTTCAGGA 2130  
Qy 562 pArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArgValle 582  
Db 2131 ATCGTACTAGACTTTA-----ATAGAGTTTGGA----- 2161  
Qy 582 uAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAlaLeu 602  
Db 2162 -----GGGACCATATCGCATGAAATTTCTCGAGTAATC----- 2197  
Qy 602 uCysHisLeuLysTyLeuSerIleGlyTySerSerIleTySerLeuProArgSe 622  
Db 2198 -----TAGCAACATCCGGTATCTAC-TCTGTATTCATTTACCTGAGAA 2243  
Qy 622 rIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyIleAlaAla 642  
Db 2244 T-----AGTTAGTAGAATTTCCAGCAGAGAAAGCCAAAGGCTCGAATCACCAT 2297  
Qy 642 uProSerGlu-----IleSerLysLeuGlnCysLeuHisThrLeuArgCys11 658  
Db 2298 TCCGTAGATCTTTTGCCCAATGAAGAGTTGAGACTTCT----- 2340  
Qy 658 eGlyGlnPheHisTyAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnTh 678  
Db 2341 -----CAGATTAATACGTGGAACTGGAAGGAGATCTTAAACTTCTCCATCTGA 2390  
Qy 678 rIle-----CysLeuProLysValPheThrProLeu-----ValSerArgAspAsp 694  
Db 2391 ACTCAAGTGTATACAGTGAAGGTTTC-----CCATTAGAAATCTCCTCCGATATTTCT 2447  
Qy 694 gAlaLysGlnIleAlaGluLeuHisMetAlaThrLysSerCysTrpSerGluSerIleG1 714  
Db 2448 TTCTAGCAACTTGGGTCTTGTGATCTT-----TCAGAGAGT---GG 2486  
Qy 714 yValLysValProLysGlyIleGlyLysLeuArgAspLeuGlnValLeuGluTyValas 734  
Db 2487 AGTAAGCAGATCAGACTTTGCCCGCAAGGGGAGGAGTGAAGCTTGAAGTTGATAA 2546  
Qy 734 pIleArgArgThrSerSer---ArgAlaIleLysGluLeuGlyGlnLeuSerLysLeuAr 753  
Db 2547 TTTGCGTGTGTCACGGCTAGAACCCATCTCTGATTTATCAAAACCAATATGCACACTAGA 2606  
Qy 753 gLysLeuGlyValThrThrAsnGlySerThrLysGluLysCys----- 767  
Db 2607 AAAGCTT-----GTCTCTGAGCGATGCAACCTTCTGTGTAGGT 2645  
Qy 768 -----LysIleLeuTyAlaAlaIleGluLysLeuSerSe 779  
Db 2646 TCCTAGATCAGTTGGTAAATCTGGGAAATTCCTTCAGCTGACCTTAGAAGGTGCTCAAG 2705

Qy 779 rLeuGlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeuGluCysLe 799  
Db 2706 TCTTTCTGAATTTCTGGGATGTTTCTGGA-----CTGAAGTGTCT 2747  
Qy 799 uAsp-----SerIleSerSerProPro----- 806  
Db 2748 TGAATAATTTTCTCTCTCTGCTGCTTCAATCTGAGTGTCTTACCAGAAACATTTGGTTC 2807  
Qy 807 ----ProLeuLeuArgThrLeuValLeuAspGlyIle----- 817  
Db 2808 CATGCCATGTTTGAAGAGCTTCTTCTGTGGAACCTCGCATAGTAAGTAACATTACCGTACTC 2867  
Qy 818 -----LeuGluG1 820  
Db 2868 TATTTTTCGCTCCAAAAGCTTGAAGCTTAGTCTTAATGGGTTCGAGGTCTATTGAAGA 2927  
Qy 820 uMetProAsnTrpIleGluGlnLeuThrHisLeuLysIleTyLeuLeuArgSerLy 840  
Db 2928 GCTACCTTCGTGTGAGGATATTTGACATCGCTCGAAGATTTATATCTTGTGATGACTGC 2987  
Qy 840 sLeuLysGluGlyLysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetValLeuHi 860  
Db 2988 ATTGCGAAACCTTCCTAGTTCT-----ATTGGAGATCTAAATAATCTCCAGAAGCTGCA 3041  
Qy 860 sLeuTyArg-----AsnAlaTyrLeuGlyG1 869  
Db 3042 TCTGATGCGCTGACGCTCCCTTTCTACGATTCCTGAGACTATAATAAGCTCATGTCA 3101  
Qy 869 uLysLeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeuTrpIleTyfGluLe 889  
Db 3102 GAAGGAATTTATTCATCAATGGAAGC----- 3126  
Qy 889 uAspGlnLeuArgGluLeuArgPheGluAspGlySerSerProLeuLeuGluLysIleG1 909  
Db 3127 ----GGGTTGGAGGAGTACCTATAGAACCGGCTCACTCTCTATGTTGAGTCACTCTC 3182  
Qy 909 uIleGlyCysArgLeuGluSerGlyIleThrGlyIleHisLeuProLysLeuLy 929  
Db 3183 TCAGGAGATTGCAAAATTT-----CTGAA 3206  
Qy 929 sGluIleProIleArgTyfGlySerLysValAlaGlyLeuGlyGlnLeu 945  
Db 3207 ACAGGTTCCG-----AGTCAATTTGGTGGATTAAATTCCTCT 3243

## RESULT 7

US-11-031-206-101  
; Sequence 101, Application US/11031206  
; Publication No. US20060031959A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Odell, Joan T.  
; APPLICANT: Meyers, Blake  
; APPLICANT: Thorpe, Catherine  
; APPLICANT: Weng, Zude  
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
; TITLE OF INVENTION: Stress Response  
; FILE REFERENCE: BB1357 US NA  
; CURRENT APPLICATION NUMBER: US/11/031,206  
; CURRENT FILING DATE: 2005-01-07  
; PRIOR APPLICATION NUMBER: US/09/566,394  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: 60/133038  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133042  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: 60/133427  
; PRIOR FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: 60/133437

```

, PRIOR FILING DATE: 1999-05-11
, PRIOR APPLICATION NUMBER: 60/133428
, PRIOR FILING DATE: 1999-05-11
, PRIOR APPLICATION NUMBER: 60/133438
, PRIOR FILING DATE: 1999-05-11
, PRIOR APPLICATION NUMBER: 60/133436
, PRIOR FILING DATE: 1999-05-11
, PRIOR APPLICATION NUMBER: 60/137667
, NUMBER OF SEQ ID NOS: 208
, SOFTWARE: Microsoft Office 97
, SEQ ID NO 101
, LENGTH: 2382
, TYPE: DNA
, ORGANISM: Zea mays
US-11-031-206-101

```

Alignment Scores:		
Pred. No.:	6.22e-21	2382
Score:	.309-00	185
Percent Similarity:	38.0%	154
Best Local Similarity:	20.8%	311
Query Match:	5.9%	241
DB:	9	38
		Length:
		Matches:
		Conservative:
		Mismatches:
		Indels:
		Gaps:

US-10-656-394A-8 (1-1032) x US-11-031-206-101 (1-2382)

Qy	218	ProCysAsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLeuLysAsp	237
Db	2	CCACGGCGTCCGGAAGTAGTACCAATTCAGACACCTCGAACACAGTGGAGATCGACGAGACT	61
Qy	238	MetIleArgGlnLeuGlyProSerSerLeuAspGlnLeuLeuGlnGluLeuGlnGly	257
Db	62	ATCTCCGATAGCTTAATTTGCCATGGAATGAATCAGAGATAGTTCAGAAA	112
Qy	258	LysValValValGlnValHisIleuSerGluTrpLeuIleGluLeuLysGlnLys	277
Db	113	-----CGGCGCAGATTCTCTATTGAAGGCATCGGCCAGGAAA	148
Qy	278	ArgTyrPheValValLeuAspAspLeu-----TrpIleLeuHisAspTrpAsnTrp	294
Db	149	AGATTCTTATTGCTACTTGTGATGACGTAGGAAGAGATTCCGACTGGAGGAT	199
Qy	295	IleAsnGluIleAlaPhePro--LysAsnAsnLysLysGlySerArgIleValIleThr	313
Db	200	-----GTCCGTATCCCACTCCGACACGAAAGACCCAAAGCTGATCTCGTACA	250
Qy	314	ThrArgAsnValAspLeuAlaGlnLysCysAlaThrAlaSerLeuValTyrHisLeuAsp	333
Db	251	TCACGTTTCCAAGAAGTAGTGTTCAGATGTTGCACAGAGAGCGCATTTGAAATGAAG	310
Qy	334	PheLeuGlnMetAsnAspAlaIleThrLeuLeuLeuArgLys--ThrAsnLysAsnHis	352
Db	311	GTTTTTCGATGATAATGCTGCTCGAACCTGTTCTTGAGCAAGCTGACACAGCGCTTTT	370
Qy	353	GluAspMetGluSer-----AsnLysAsnMetGlnLysMetValGluArgIleVal	369
Db	371	GCACGACTTTCAGTCCCGAATTTCAACAAGGTTGTTTCGGGACAGGCGCAGGAAAAATATTC	430
Qy	370	AsnLysCysGlyArgLeuPheLeuAlaIleLeuThrIleGly--AlaValLeuAlaThr	388
Db	431	TCCAGTTGTGGAGGCTACCACTTCCATTCATTTGGAGCTGCTGTGGCAGGGTTT	490
Qy	389	LysGlnValSerGluTrpGlnLysPheTyrGluHisLeuProSerGluLeuGluIleAsn	408
Db	491	GAAGGCCAAGATGGATTTCAGCTGCTAATGCATC-----AATATGTTTCAGCAAT	544
Qy	409	ProSerLeuGluAlaLeuArgArgMetValThrLeuGlyTyrAsnHisLeuProSerHis	428
Db	545	GAAGATGTGGATGAAATGTTTATCCGCTGGTAAATACACGACTATGACGGCTGAATTCAC	604
Qy	429	LeuLysProCysPheLeuTyrLeuSerIlePheProGluLeuPheGluIleLysArgAsn	448

605 CAACAACAGTGCCTTTTGTACTGCACCTCTTTTCCCGAAGATGATGATCTATTATGTAAGAA 664

449 ArgLeuValGlyArgTrpIleAlaGluGlyPheValArgProLysValGlyMetThrThr 468

665 CCAATTAGTTGATTTTGGCTGGCTGAAGGTTTGGCTT-----CTCAATGAT 709

469 LysAspValGlyGluSerTyrPheAsnGluLeuLeuLeuAsnArgSerMetIleGlnArgSer 488

710 CQTCAAAAGGTGATCAGATAATTACAGACCTTATTTCAGCATGCTGTGTCGACACCGGT 769

489 ArgValGlyIleAlaGlyLysIleLysThrCysArgIleHisAspIleIleArgAspIle 508

770 AGC---TCATTGTCTCAAAAGTAA---ATGCACCATGTGTAATCAGGCATATG 817

509 ThrVal---SerIleSerArgGlnGluAsnPheValLeuLeuProMetGlyAspGlySer 527

818 GCGATTGTTGGTTTACACAGACAGATCAAAAGTTCTTCGTTCAAGCAGGATCGCTTGT 877

528 AspLeuValGlnGluAsnThrArgHisIleAlaPheHisGlySerMetSerCysLysThr 547

878 GAT-----AGTGCTCCACCA 892

548 GlyLeuAspTrpSerIleIleLeuArgSerLeuAlaIlePheGlyAspArgProLysSerLeu 567

893 CGACAAGAGTGAAGGAATCGACACAGATCTCCATCATGCTCTAATGATATCAAAAGAGCTT 952

568 AlaHisAlaValCysProAspGlnLeuArgMetLeuArgValLeuAspLeuGluAspVal 587

953 CCTTCTTCACCG-----GAATGTGAANAACCTC 979

588 ThrPheLeuIleThrGlnLys-----AspPheAspArgIleAla----- 600

980 ACTACATTGTTGATCCAAATAACCCAAATTTGAACACAGCTGAGTTCAGGCTTTTTCAGG 1039

601 LeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSerSerIleTyrSerLeuPro 620

1040 TTTATGCCCTCCTTGAAGAGTGTGATCTTTCTCAC---ACTGCATTAACAACTGCCA 1096

621 ArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAla 640

1097 ---GAATGTGAGACATTGGTTGCAATACAGCATCTCAATTTGTCACACACAGTATTAGG 1153

641 AlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGln 660

1154 TTATTACCT-----GAGCGCTGTGTTATTGAAGAGTTGAGG----- 1192

661 PheHisTyrAspAsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCys 680

1193 ---CATCTGGAT----- 1201

681 LeuProLysValPheThrProLeuValSerArgAspArgAlaLysGlnIleAlaGlu 700

1202 -----CTCAGCGTGACTGCTGAA 1219

701 LeuHisMetAlaThrLysSerCysTrpSerGluSerIleGlyValLysValProLys--- 719

1220 CTCGAAGATACCTTGAACACTGC---TCAAGGTACTCAATTTAAGAGTTCTTAATCTC 1276

720 -----GlyIleGlyLysLeuArgAsp-----LeuGlnVal 729

1277 TTTCGAGTCACTATGTTATTAGTACGCTCAACGACTCGAATCTGGAATCTCCCTGAAGSCA 1336

730 LeuGluTyrValAspIleArgArgThrSerSerArgAlaIleLysGluLeuGlyGlnLeu 749

1337 CTGATGTTCTTGGAACTCACTATTATTATACAGAGAAGGTGTTAAAGAAACTGAACAAGACT 1396

750 SerLysLeuArgLysLeuGlyValThrThrAsnGlySerThr----- 763

1397 AGTCCTTTGGCAAG-----TCAACATATCTGCTGCATCTTAAG 1435

764 -----LysGluLysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLeuGln 781

1436 TACTGTGAGAAGAAATCGACTCGATCAAAATCTCGCATCTCGACACTTGTGTCAACTCGAG 1495

Qy 782 SerLeuHisValAspAlaAlaGlyIleSerAspGlyThrLeuGluCysLeuAspSer 801  
Db 1496 GAGCTGATGTCGAATCA-----TCTATAAT--- 1522  
Qy 802 IleSerSerProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGluGluMet 821  
Db 1523 -----CTAAACACTCTTGTGCTGATGCTGAGCTGAGCGGCATCA 1561  
Qy 822 ProAsnTrpIleGluInLeuThr----- 829  
Db 1562 GATTGAGCGCTGAGCTCTCAGCTTCTGCTGCTGAGAGACGTCATTGTT 1621  
Qy 830 -----HisLeuIleValLeuIleValLeuLeuArg-----SerIys 840  
Db 1622 GCACCAAGCGCCCAACATTTTCAGCAGATCGCAATTTGACCATTCGATTCGCCCAAG 1681  
Qy 841 LeuLeuGluGlyIleValLeuMetLeuGlyAlaLeuProAsnLeuMetValLeuHis 860  
Db 1682 TTGAAGAAACATCATGCGTCTCTAAACTTGAATGCTCGAGAGCGCTCGTGTGATCCAT 1741  
Qy 861 Leu-----TyrArgAsnAlaIleTyr 866  
Db 1742 TGTGATGGTGTGCTGAAGATTCTGAAGACAGACCGGTGATGAGCGAGAAACAACAAATG 1801  
Qy 867 LeuGlyGlu-----LysLeu 871  
Db 1802 TTGGTTCAGGCTCATCTTCTGAAGACAGGAGATAAAGGATTGATGTCGTCAAAGT 1861  
Qy 872 ValPheIleThr-----GlyAlaPheProAsnLeuArgThrLeuTrpIle 886  
Db 1862 GTGTGAAGAGCGATGACAAATGTCATGCTGAGCTCTGAACTCGAGATCAATCGTGTG 1921  
Qy 887 TyrGluLeuAspGlnLeuArgGluIleArgPheGluAspGlySerSerProLeuLeuGlu 906  
Db 1922 ACTGATGTCAGAGCGCTGAGAGATATC---TGCAAGCCAGAAATTTTCCAGCTCGAG 1978  
Qy 907 LysIleGluIleGlyCysArgLeuGluSerGlyIleThrGlyIleIleHisLeuPro 926  
Db 1979 ACCATCGGGTGGAGGATGTC-----CCG 2002  
Qy 927 LysLeuLysGluIleProIleArgTyrGlySerLysValAlaGlyLeuGlyGlnLeuGlu 946  
Db 2003 AATCTGAAGAGCATCCATGAGCAGCAGTACACTGTGGAACTGAGCAGGTCGTC 2062  
Qy 947 GlyGluVal-AsnAlaHisProAsnArgProValLeuLeuMetTyrSerAspArgTyr 966  
Db 2063 GGTTCAGTTGAATGTTGGGAGAAAC-----TGGAGTGGGAGGACA-- 2102  
Qy 966 rHisAspLeuGlyAlaGluAlaGluGlySerSerIleGluValGlnThrAlaAspProVa 986  
Db 2103 -----AGGAGGCGAAGGAGAGAGAGTCTTTCATCTGACAGGCCCT 2149  
Qy 986 lProAsp-----AlaGluGlySerValThrValAlaValGluAlaThrAs 1001  
Db 2150 CCGCGCCCTCGCTTACGTGTTCTCGCGGTTGCTTGTCTGAGTGGCAGGAGCTCGTTC 2209  
Qy 1001 pProLeuProGluInGluGlyGluSerSer 1011  
Db 2210 AATGCTGCCACGNAATAGCGGTTCGGAATCT 2240

RESULT 8

US-11-031-206-107  
; Sequence 107, Application US/11031206  
; Publication No. US20060031959A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Faico, Saverio Carl  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Odell, Joan T.  
; APPLICANT: Meyers, Blake

APPLICANT: Thorpe, Catherine  
APPLICANT: Weng, Zude  
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
FILE REFERENCE: BB1357 US NA  
CURRENT APPLICATION NUMBER: US/11/031.206  
CURRENT FILING DATE: 2005-01-07  
PRIOR APPLICATION NUMBER: US/09/566,394  
PRIOR FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: 60/133038  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: 60/133042  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: 60/133427  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133437  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133428  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133438  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133436  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/137667  
PRIOR FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 107  
LENGTH: 644  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (277)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (415)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (471)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (487)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (495)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (497)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (511)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (585)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (599)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (605)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (610)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (639)  
US-11-031-206-107  
Alignment Scores:  
Pred. No.: 1.37e-20  
Score: 298.00  
Percent Similarity: 59.0%

Length: 644  
Matches: 63  
Conservative: 39

Best Local Similarity: 36.4% Mismatches: 57  
 Query Match: 5.7% Indels: 14  
 DB: 9 Gaps: 4

US-10-656-394A-8 (1-1032) x US-11-031-206-107 (1-644)

QY 375 LeuProLeuAlaIleuThrIleGlyAlaValLeuAlaThrLys--GlnValSerGlu 393  
 DB 1 CTGCCACTAGCAATTTTACAGTGGCAGCTGTCTGTCTCACTAGACACCAATAACATT 60  
 QY 394 TrpGluLysPheTyGluHisLeuProSerGluLeuGluLeuLeuProSerLeuGluAla 413  
 DB 61 TGGAAATCAACATACCAACAGCTTCGAGTGTGAGTGTCAACCAAT-----GATCAT 111  
 QY 414 LeuArgMetValThrLeuGlyTyraHisLeuProSerHisLeuLysProCysPhe 433  
 DB 112 GTCCGAGCAATCTTAATCTAAGCTACCATCTATCTGAGATCTCAGAACTGCTTC 171  
 QY 434 LeuTyLeuSerIlePheProGluAspPheGluLeuLysArgAsnArgLeuValGlyArg 453  
 DB 172 TTGTATTCAGCTTTCTTCTGAAGACTACCCATGTACCGAAGCCCTTGTGCGGCTC 231  
 QY 454 TrpIleAlaGluGlyPheValArgProLysValGlyMetThrThrLysAspValGlyGlu 473  
 DB 232 TGGGTTCGCAAGAGTTTCTTCTGAGTAAGAAGAATACACCNAGGAGGTGGCTGAG 291  
 QY 474 SerTy-PheAsnGluLeuLeuAsnArgSerMetIleGlnArgSerArgValGlyIleAla 493  
 DB 292 GGAATCTCATGGAATTTGATCCACGTAATATGCTTGAAGTTGTAGACTATGATGAGTT 351  
 QY 494 GlyLysIleLysThrCysArgIleHisAspIleLeuArgAspIleThrValSerIleSer 513  
 DB 352 GGCAGGGTTAGCACTTGCAGATGTCATGATATCATGAGGACCTGGCACCTTTGTGTGCC 411  
 QY 514 ArgGlnGluAsnPheValLeuLeuProMetGlyAspGlySerAspLeu-----529  
 DB 412 AANAAGAGAGTTT-----GGTCTGCAACAGGATTTATGTTGAACTGATA 456  
 QY 530 ---ValGlnGluAsnThrArgHisIleAlaPheHisGly 541  
 DB 457 CAGGTGGACCAAGAGTTTGTGCTGCTTGTGCTGATGTTGCTGATGTTGCTG 495

RESULT 9

US-11-096-568A-34295  
 ; Sequence 34295, Application US/11096568A  
 ; Publication No. US20060048240A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nikolai et al.  
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 ; TITLE OF INVENTION: Therby  
 ; FILE REFERENCE: 2750-1592PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096,568A  
 ; CURRENT FILING DATE: 2005-04-01  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO 34295  
 ; LENGTH: 4585  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(4585)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 13605763  
 US-11-096-568A-34295

Alignment Scores:  
 Pred. No.: 1,89e-14 Length: 4585  
 Score: 250.00 Matches: 204  
 Percent Similarity: 36.8% Conservative: 146  
 Best Local Similarity: 21.4% Mismatches: 298  
 Query Match: 4.7% Indels: 304  
 DB: 9 Gaps: 56

US-10-656-394A-8 (1-1032) x US-11-096-568A-34295 (1-4585)

QY 72 IleArgAspLeuSerTyAspIleGluAspSerLeuAspGluPheLysValHisIleGlu 91  
 DB 61 GTAAAGATGTCCTTCATCATGATAGCATGATTCCTTTCCAAC-----GAG 105  
 QY 92 SerGlnThrLeuPheArgGlnLeuValLysLeuArgHisArgIleAlaIle--- 110  
 DB 106 TCTCAATCAATGGTC-----GAGAGACTAGGGTTTCTGTATG 144  
 QY 111 -----ArgIleHisAsnLeuLysSerArgValGluGluValSerArg 125  
 DB 145 ATTTTACCAGGAACCGTACGGTATCTTTGACAAGCTCGTGAAGTCTTCGATGCCAG 204  
 QY 126 AsnThrArgTySerLeuValLysProIle-----SerSerGlyThrGlu 140  
 DB 205 AAGAAACAAGATCAAGTGTGTTCGGTGTGTTCAGGTGTGATCAGATCATCAGAGCCGAA 264  
 QY 141 -----IleAspMetAspSerTyAla----- 147  
 DB 265 TGGCTTAGCGCGCTGGATTCGAAGGATTCATCATGATACCATTCAGAGAAAGATGT 324  
 QY 148 -----GluAspIleArgAsnGlnSerAlaArgAsnValAspGlu-----Ala 161  
 DB 325 AGTGACTCCAGCTTGTAAAGAGAGACTGTGTAGAGATGTGTATGAGAGAGCTCTTTTATATG 384  
 QY 162 GluLeuValGlyPheSerAspSerLysLysArgLeuLeuMetIleAspThrAsnAla 181  
 DB 385 GAACGATTTGGATA-----TATTCGAGCTGTCTGGAG---ATTGAGAAATGATT 432  
 QY 182 AsnAspGlyProAlaLysValIleCysVal-----ValGlyMetGlyLysLeuGlyLys 199  
 DB 433 AACAGCAACACCTTGGACATCCGTGTGTGTGAATTTGGGTATGCTGTCATAGCAAG 492  
 QY 200 ThrAlaLeuSerArgLysIlePheGluSerGluGluAspIleArgLysAsnPheProCys 219  
 DB 493 ACTACACTTGTCTAAAGCAGTCTTTGACCA----- 522  
 QY 220 AsnAlaTrpIleThrValSerGlnSerPheHisArgIleGluLeuLysAspMetIle 239  
 DB 523 -----ATGCTGTGAGTTCATGCTCATTTGATTAAGACTACACC 567  
 QY 240 Arg-----GlnLeuLeuGlyProSerSerLeu-----AspGlnLeuLeuGlnGluLeu 255  
 DB 568 AAAGCTATTCAAGAGAGGGTGTATTGTGTGTGGAGGAGACAGTTTTTGAAGAAAT 627  
 QY 256 GlnGlyLys-----ValValGlnValHisIleSerGluTyLeuIleGluGlu 273  
 DB 628 GCTGTGTGTAGTGTACCGTTACGAAATTTG-----AGCTTGTCTTAGGGATAGA 675  
 QY 274 LeuLysGluLysArgTyPheValValLeuAspAspLeu----- 286  
 DB 676 TTAACAATAAGAGGGTCTTGTGTCTTGTATGATGTCGCGAGTCTCTGTGTGTGGAG 735  
 QY 287 TrpIleLeuHisAspTrpAsnTrpIleAsnGluIleAlaPheProLysAsnAsnLysLys 306  
 DB 736 TCTTTTCTTGGAGGGTTTGACTGTTTGTGT-----CCCAAA----- 771  
 QY 307 GlySerArgIleValIleThrThrArgAsnValAspLeuAlaGluLysCysAlaThrAla 326  
 DB 772 ---AGTCTAATCATCATACCTCAAGATAAATCGGTGTTCGCTTGTGT---CGAGTC 825  
 QY 327 SerLeuValTyThrHisLeuAspPheLeuGlnMetAsnAspAlaIleThrLeuLeuArg 346  
 DB 826 AATCAATATACGAGGTTCAGGGTTTAAATGAGAAAGAGGCTCTTCAACTCTTC- 879  
 QY 347 LysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsnMetGlnLysMetValGlu 366  
 DB 880 TCTTTGTGTGCGTCTATAGACCATATG---GCAGAGCAGAAATCTCCAGAGGTGCAATG 936  
 QY 367 ArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeu 386  
 DB 937 AAGTTATTAAATATCTAATGCGCATCCATTAGCTCTCAATCTCTATGTCAGAGAACTG 996



QY 387 AlaThrLysGlnValSerGluTrpGluLysPheTyrGluHisLeuProSerGluLeuGlu 406  
DB 997 ATGGGAAGAA-  
QY 407 Ile-  
DB 1027 ATAGCATTCCTCAAACTCAAGAAATGCTCTCCAGCTATTTTGTGATCAATCAAGAGC 1086  
QY 417 MetValThrLeuGlyTyrAsnHisLeuProSerHisLeuLysProCysPheLeuTyrLeu 436  
DB 1087 -TCGTATGACACACTCAATGACAGGGAATAAATTTTGTGCACATA 1134  
QY 437 SerIlePhe-  
DB 1135 GCTGTGTTCTTCAGGAGAAATGTTGACTGATGATGACGCTCTTGAGGGTGT- 1191  
QY 455 IleAlaGluGlyPheValArgProLysValGlyMetThrThrLysAspValGlyGluSer 474  
DB 1192 -GGTTTCTTT-CCACATGTTGGAATT- 1221  
QY 475 TyrPheAsnGluLeuLeuAsnArgSerMet-  
DB 1222 -CTGTGGAGAGAGCTGTTGACTGATGATGACGCTCTTGAGGGTGT- 1263  
QY 493 AlaGlyLysIleLysThrCysArgIleHisAspIleIleArgAspIleThrValSerIle 512  
DB 1264 -CGATGCATAACTTGATCCCAAGATGT- 1290  
QY 513 SerArgGlnGluAsnPheValLeuLeuProMetGlyAspGlySerAspLeuValGlnGlu 532  
DB 1291 -GCGCGCAAAATAATAATAGA 1311  
QY 533 AsnThrArgHisIleAlaPheHisGlySerMetSerCysLysThrGlyLeuAspTyrSer 552  
DB 1312 GAAACAGACAGACTAAGAGCGCCAGCAGACTG- 1350  
QY 553 IleIleArgSerLeuAlaIlePheGlyAspArgProLys- 565  
DB 1351 CCTTGCAGCTCAAAATATTATTAGAGATAAGGACAAACGAAATAGAACACAAAA 1410  
QY 566 -SerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeuArgValLeuAspLeu 584  
DB 1411 ACAACTTTGAAGCTGCTCAGGCTCCCTGAAGAGATCGAAGCATG- 1467  
QY 595 GluAspValThrPheLeuIleThrGlnLysAspPheAspArgIleAlaLeuLeuCysHis 604  
DB 1468 TCNAACCTAAGTTTGTATATTAGCATGTTGCTTTGATATATATATGTAACCTTAGATTG 1527  
QY 605 LeuLysTyrLeuSerIleGlyTyrSerSerIleTyrSerLeuProArgSerIleGly 624  
DB 1528 TTCAAG- 1560  
QY 625 LysLeuGlnGlyLeuGlnThrLeuAsnMetProSerThrTyrIleAlaAlaLeuProSer 644  
DB 1561 CATGTAAAC- 1605  
QY 645 GluIleSerLysLeuGlnCysLeuHisThrLeuArgCysIleGlyGlnPheHisTyrAsp 664  
DB 1606 GTGCTAAGACTCTG- 1629  
QY 665 AsnPheSerLeuAsnHisProMetLysCysIleThrAsnThrIleCysLeuProLysVal 684  
DB 1630 AACTATCTCTGCAGTTT- 1659  
QY 685 PheThrProLeuValSerArgAspArgAlaLysGlnIleAlaGluLeuHisMet- 703  
DB 1660 TTTCATCTATA- 1695  
QY 704 -AlaThrLysSerCysTyrSerGluSerIleGlyValLysValProLysGlyIle 721  
DB 1696 TACGCCCAACTTGAACCTTTGG- 1719  
QY 722 GlyLysLeuArgAspLeuGlnValLeuGluTyrValAspIleArgArgThrSerSerArg 741

DB 1720 GGTGAACCAAGGACCTGGAGATGTTGAAG- 1773  
QY 742 AlaIleLysGluLeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThr- 760  
DB 1774 CAACTGTGATATGACATCTTTTAAAGCTCAAAATCTTGAGGTGATGATCTCAA 1833  
QY 761 GlySerThrLysGluLysCysLysIleLeuTyrAlaIleGluLysLeuSerSerLeu 780  
DB 1834 GGCTGTACA- 1857  
QY 781 -GlnSerLeuHisValAspAlaAlaGlyIleSerAspGlyGlyThrLeu 796  
DB 1858 CCAGCCACCGGTCAATGCTACATTTACAGTGTGAATCTCTCAGGT- 1905  
QY 797 GluCysLeuAspSerIleSerPro- 814  
DB 1906 -TGACACAGAGATCAAAAGTTTCCAGAAAATCCCAAAATATTGACACTGAATCTA 1962  
QY 815 AspGlyIle- 833  
DB 1963 CAGGGACTGTGATATGATGATTTACACTTTCCATTTGTAATTCCTGGAGCTGAATGAT 2022  
QY 834 IleTyrLeuLeuArgSerLysLysGluGlyLysThrMetLeuIleLeuGlyAlaLeu 853  
DB 2023 TGTTCGTGTTGCGAAGT- 2043  
QY 854 ProAsnLeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLysLeuValPhe 873  
DB 2044 CCAACATGGTTAATTTAGAACTTCTCAAGCCCTTGATCTTTCTGGTGTCTGAGCTC 2103  
QY 874 LysThr- 887  
DB 2104 GAGACTATCCAGGTTTCCACGGAACCTGAAGAGTTATATCTTTGTTGGCAGCTG 2163  
QY 888 -GluLeuAspGlnLeuArgGluLeuArgPheGluAspGlySerSerPro 903  
DB 2164 AGCAAGTGCCCAACTTCTCAAGTCTAGAAATCTTTAATGCCCATGGTGTG- 2217  
QY 904 LeuLeuGluLysIleGluIleGlyCysArgLeuGluSerGlyIleThrGlyIle 923  
DB 2218 -GTCTCTCAAAATCAATTCGTTTGAC- 2244  
QY 924 HisLeuProLysLeuLysGluIleProIleArgTyr 935  
DB 2245 -TTCAAGAGAGCTTCTGTGATTCATAC 2268  
RESULT 10  
US-11-031-206-133  
Sequence 133, Application US/11031206  
Publication No. US20060031959A1  
GENERAL INFORMATION:  
APPLICANT: Rafalski, Antoni  
APPLICANT: Miao, Guo-Hua  
APPLICANT: Falco, Saverio Carl  
APPLICANT: Sakai, Hajime  
APPLICANT: Famodu, Omolayo O.  
APPLICANT: Odell, Joan T.  
APPLICANT: Meyers, Blake  
APPLICANT: Thorpe, Catherine  
APPLICANT: Weng, Zude  
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
TITLE OF INVENTION: Stress Response  
FILE REFERENCE: BB1357 US NA  
CURRENT APPLICATION NUMBER: US/11/031,206  
CURRENT FILING DATE: 2005-01-07  
PRIOR APPLICATION NUMBER: US/09/566,394  
PRIOR FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: 60/133038  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: 60/133042  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: 60/133427

PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133437  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133428  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133438  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133436  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/137667  
PRIOR FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 133  
LENGTH: 629  
TYPE: DNA  
ORGANISM: Triticum aestivum  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (511)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (523)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (542)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (547)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (549)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (557)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (595)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (602)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (610)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (622) .. (623)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (629)  
US-11-031-206-133

Alignment Scores:  
Pred. No.: 2,31e-14  
Score: 237.50  
Percent Similarity: 55.0%  
Best Local Similarity: 35.0%  
Query Match: 4.5%  
DB: 9  
Gaps: 5

US-10-656-394A-8 (1-1032) x US-11-031-206-133 (1-629)

Qy 284 AspAspLeuThrTrpLeuHisAspTrpAsnTrpLeuGlnLeuAlaPheProLysAsn 303  
Db 2 GATGATGTGGGAATCCAGACATATGCTGATGTCAGT---GCATTT-----CAG 52  
Qy 304 AsnLysLysGlySerArgIleValIleThrTrpArgAsnValAspLeuAlaGluLysCys 323  
Db 53 GGTCTCCAGGAAGCGGTGTATGATCAGCAGCGGGAAGATGTGCG---GCTCTT 109  
Qy 324 AlaThrAlaSerLeuValTrpHisLeuAspPheLeuGlnMetAsnAspAlaIleThrLeu 343  
Db 110 GCTCTAGTGAGCGCGTCGCCTACAACTCCAGCCATTTGGTAGGACGAGTCATTTCAAGCTA 169

Qy 344 LeuLeuArgLysThrAsnLysAsnHisGluAspMetGluSerAsnLysAsnMetGlnLys 363  
Db 170 TTCTGCTCAAGGGCTTTCCACACACCCCTAGACCGCAAGTCCCTCCGAGGCTTGAGAG 229  
Qy 364 MetValGluArgIleValAsnLysCysGlyArgLeuProLeuAlaIleLeuThr-IleG1 383  
Db 230 GTGGCTGTGATGTAGTTAAGAGGTGTATGCGCTCCCATTTGACCATTTGATCTCTCTGG 289  
Qy 383 yAlaValLeuAlaThrLysGlnValSerGlu-----TrpGluLysPheTrpGluHisLe 401  
Db 290 CAGCTATTGTCACGAAGCAGCCGACACAGCAGCTTGGAAATCATGTACATCATCT 349  
Qy 401 u-ProSerGluLeuGluLeuAsnProSerLeuGluAlaLeuArgMetValThrLeuG 421  
Db 350 CCGGAGCGCAACTACAGGCAATAACCATGTCACAGCTAIA-----CTTATCTGA 400  
Qy 421 lyTyAsnHisLeuProSerHisLeuLysProCysPheLeuTrpLeuSerIlePheProG 441  
Db 401 GCTACCATGACTTGCAGAGGTGATCTCAAGAACTGCTCCTGACTGACGCTTGTTCCTG 460  
Qy 441 luAppPheGluIleLysArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPhe 459  
Db 461 AAGACTATGCAATGTCACGGGAGAACTTGTGCGGTTGTGGGTGCTGANGGTTTC 516

RESULT 11

US-11-031-206-139  
Sequence 139, Application US/11031206  
Publication No. US20060031959A1  
GENERAL INFORMATION:  
APPLICANT: Rafalski, Antoni  
APPLICANT: Miao, Guo-Hua  
APPLICANT: Falco, Saverio Carl  
APPLICANT: Sakai, Hajime  
APPLICANT: Famodu, Omolayo O.  
APPLICANT: Odell, Joan T.  
APPLICANT: Meyers, Blake  
APPLICANT: Thorpe, Catherine  
APPLICANT: Weng, Zude  
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
FILE REFERENCE: BB1357 US NA  
CURRENT APPLICATION NUMBER: US/11/031,206  
PRIOR FILING DATE: 2005-01-07/566,394  
PRIOR APPLICATION NUMBER: US/09/566,394  
PRIOR FILING DATE: 2000-05-05  
PRIOR APPLICATION NUMBER: 60/133038  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: 60/133042  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: 60/133427  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133437  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133428  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133438  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/133436  
PRIOR FILING DATE: 1999-05-11  
PRIOR APPLICATION NUMBER: 60/137667  
PRIOR FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 208  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 139  
LENGTH: 634  
TYPE: DNA  
ORGANISM: Triticum aestivum  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (378)  
FEATURE:  
NAME/KEY: unsure

LOCATION: (420)  
 NAME/KEY: unsure  
 LOCATION: (456)  
 FEATURE: (456)  
 NAME/KEY: unsure  
 LOCATION: (495)  
 FEATURE: (495)  
 NAME/KEY: unsure  
 LOCATION: (498)  
 FEATURE: (498)  
 NAME/KEY: unsure  
 LOCATION: (506)  
 FEATURE: (506)  
 NAME/KEY: unsure  
 LOCATION: (546)  
 FEATURE: (546)  
 NAME/KEY: unsure  
 LOCATION: (561)  
 FEATURE: (561)  
 NAME/KEY: unsure  
 LOCATION: (567)  
 FEATURE: (567)  
 NAME/KEY: unsure  
 LOCATION: (577)  
 FEATURE: (577)  
 NAME/KEY: unsure  
 LOCATION: (581)  
 FEATURE: (581)  
 NAME/KEY: unsure  
 LOCATION: (583)  
 FEATURE: (583)  
 NAME/KEY: unsure  
 LOCATION: (599)  
 FEATURE: (599)  
 NAME/KEY: unsure  
 LOCATION: (615)  
 FEATURE: (615)  
 NAME/KEY: unsure  
 LOCATION: (621)  
 FEATURE: (621)  
 NAME/KEY: unsure  
 LOCATION: (623)  
 FEATURE: (623)  
 US-11-031-206-139

Alignment Scores:  
 Pred. No.: 4.55e-13 Length: 634  
 Score: 225.00 Matches: 58  
 Percent Similarity: 52.4% Conservative: 28  
 Best Local Similarity: 35.4% Mismatches: 48  
 Query Match: 4.3% Indels: 30  
 DB: 9 Gaps: 6

US-10-656-394A-8 (1-1032) x US-11-031-206-139 (1-634)

Qy 368 ILeValAsnLysCysGlyArgLeuProLeuAlaIleLeuThrIleGlyAlaValLeuAla 387  
 Db 3 ATAGTTGATAGGTGTCATGCTACCTCTAGCAATTTGTTACCATTTGGTGCATGTTGCT 62  
 Qy 388 ThrLysGln---ValSerGluTrpGluLysPheTyrgluHisLeuProSerGluLeuGlu 406  
 Db 63 TCAAGACAACGATTAGACATTTGGAATCAAAATACAAATCAGCTTCGAAGCGAGTTGTCA 122  
 Qy 407 ILeAsnProSerLeuGluAlaLeuArgMetValThrLeuGlyTyraenHisLeuPro 426  
 Db 123 AACAAAT-----GATCATGTCGACCAATTTAACTGAGCTACCATGACCTTCCA 173  
 Qy 427 SerHisLeuLysProCysPheLeuTyrgluSerIlePheProGluaspPheGluIleLys 446  
 Db 174 GACGACCTCAAAACTGTTTTTATCTGTCAGCTCTATTCCTGAGACTATCACATGTCA 233  
 Qy 447 ArgAsnArgLeuValGlyArgTrpIleAlaGluGlyPheValArgProLysValGlyMet 466

Db 234 CQTGAACCTTGGTGGCTGTGGTGGTCCGAGAGCTTGGTGGTAAAGAAAGAA 293  
 Qy 467 ThrThrLysAsp-----ValGlyGluSerTyrrPheAsnGluLeuIleAsnArgSer 483  
 Db 294 CACACCAGAGATGGGTAGCTTGGAGGAACTCC-----ATGGAT 332  
 Qy 484 MetIleGlnArgSerArgValGlyIleAla----- 493  
 Db 333 TTGATCCAAACCGCAATAGCTTTGAAGTTGTTAGAGAATGATGACTTNGTAAGTAACACCT 392  
 Qy 494 GlyLysIleLysThrCysArgIleHisAspIleLeuArgAspIleThrValSerIleSer 513  
 Db 393 GGTAAAGATCATGATATGCGCGTGAAC-----NACTAGTCGGTGTGCT 434  
 Qy 514 ArgGlnGluAsn 517  
 Db 435 AAAGAAGAAAT 446

RESULT 12

US-11-031-206-105  
 ; Sequence 105, Application US/11031206  
 ; Publication No. US20060031959A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rafalski, Antoni  
 ; APPLICANT: Miao, Guo-Hua  
 ; APPLICANT: Falco, Saverio Carl  
 ; APPLICANT: Sakai, Hajime  
 ; APPLICANT: Famedu, Omelayo O.  
 ; APPLICANT: Odell, Joan T.  
 ; APPLICANT: Meyers, Blake  
 ; APPLICANT: Thorpe, Catherine  
 ; APPLICANT: Weng, Zude

; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in  
 ; FILE REFERENCE: B01357 US NA  
 ; CURRENT APPLICATION NUMBER: US/11/031,206  
 ; PRIOR FILING DATE: 2005-01-07  
 ; PRIOR APPLICATION NUMBER: US/09/566,394  
 ; PRIOR FILING DATE: 2000-05-05  
 ; PRIOR APPLICATION NUMBER: 60/133038  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133042  
 ; PRIOR FILING DATE: 1999-05-07  
 ; PRIOR APPLICATION NUMBER: 60/133427  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133437  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133428  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133438  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/133436  
 ; PRIOR FILING DATE: 1999-05-11  
 ; PRIOR APPLICATION NUMBER: 60/137667  
 ; PRIOR FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 208  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 105  
 ; LENGTH: 1892  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays

US-11-031-206-105

Alignment Scores:  
 Pred. No.: 1.69e-10 Length: 1892  
 Score: 206.50 Matches: 133  
 Percent Similarity: 34.4% Conservative: 90  
 Best Local Similarity: 20.4% Mismatches: 138  
 Query Match: 3.9% Indels: 291  
 DB: 9 Gaps: 33  
 US-10-656-394A-8 (1-1032) x US-11-031-206-105 (1-1892)

416 ArgMetValThrLeuGlyTyrAsnHisLeuProSer---HisLeuLysProCysPheLeu 434  
|||  
Db 6 COTCCGCTCAAGAGAGTTATGATACCTGCCAGCTGACAGAGTTAAGCTCTGCCTGCTA 65  
|||  
Qy 435 TyrLeuSerIlePheProGluAspPheGluIleArgAsnArgLeuValGlyArgTrp 454  
|||  
Db 66 TATTCTCTATTGTTCCAGAGAGGTTCTTATTATTCAGAGATTGGATCATAGGCTACTGCG 125  
|||  
Qy 455 IleAlaGluGlyPheValArgProLysValGlyMetThrThrLysAspValGlyLysSer 474  
|||  
Db 126 ATCGGTGAAGGTTTCATA---GACGACTGTATAT 158  
|||  
Qy 475 TyrPheAsnGluLeuIleAsnArgSerMetIleGlnArgSerArgValGlyIleAlaGly 494  
|||  
Db 159 GAGATGGATGAATATATACAAACAGGGG--- 185  
|||  
Qy 495 LysIleLysThrCysArgIleHisAspIleIleArgAspIleThrValSerIleSerArg 514  
|||  
Db 186 ---CATGACCTTCTTGGTGATCTCAAGATTGCC--- 215  
|||  
Qy 515 GlnGluAsnPheValLeuLeuProMetGlyAspGlySerAspLeuValGlnGluAsnThr 534  
|||  
Db 216 ---TCTTTCTCGAGAAAGTGAAGATGAGGAT--- 245  
|||  
Qy 535 ArgHisIleAlaPheHis--- 540  
|||  
Db 246 ---CATATCAAGATGACCTATGTTGCGTCGTCATGCTCTGTGGATTGTCATCAGATTTC 302  
|||  
Qy 541 GlySerMetSerCysLys---ThrGlyLeu--- 549  
|||  
Db 303 GGCACCAAGGACCAATGCTGCTGCTGCTGAGTTGGCTGAAGGAGGACCAAGGC 362  
|||  
Qy 550 ---AspTrp---SerIleIleArgSer---LeuAlaIle 559  
|||  
Db 363 GCAGAGAAATGAACGATGCTGAGCGGATTTCTTCATGCGGAACCAACTTCTGAGTTG 422  
|||  
Qy 560 PheGlyAspArgProLysSerLeuAlaHisAlaValCysProAspGlnLeuArgMetLeu 579  
|||  
Db 423 TAT---GAGAGGCTTAAC---TGCCCC---TTACTG 449  
|||  
Qy 580 ArgValLeuAspLeuGluAspValThrPheLeuIleThrGlnLysAspPheAspArgIle 599  
|||  
Db 450 AAGACATTGATGCTGCAAGGA---AATCTGGGTGGACAGATA 491  
|||  
Qy 600 Ala---LeuLeuCysHisLeuLysTyrLeuSerIleGlyTyrSerSer 614  
|||  
Db 492 TGTGATGGATTCTTCAATACATACATCTCTCAGAGTTAGATCTGTCTCAT---ACC 548  
|||  
Qy 615 SerIleTyrSerLeuProArgSerIleGlyLysLeuGlnGlyLeuGlnThrLeuAsnMet 634  
|||  
Db 549 TCTATCAGCGAATTGCCCTCAGGATCAGTTTCATGTTGAGTTGAGTACCTGAGATTG 608  
|||  
Qy 635 ProSerThrTyrIleAlaAlaLeuProSerGluIleSerLysLeuGlnCysLeuHisThr 654  
|||  
Db 609 TATACACAAACATCAGGTCACTTCCAGGGAGTAGGATCTCTATCGACTCTGCGGTTG 668  
|||  
Qy 655 LeuArgCysIleGlyGlnPheHisTyrAspAsnPheSerLeuAsnHisP-ProMetLysCys 674  
|||  
Db 669 TTG--- 671  
|||  
Qy 675 IleThrAsnThrIleCysLeuProLysValPheThrProLeuValSerArgAspArg 694  
|||  
Db 672 ---CTTCTCTG--- 680  
|||  
Qy 695 AlaLysGlnIleAlaGluLeuHisMetAlaThrLysSerCysTrpSerGluSerIleGly 714  
|||  
Db 681 ---CATATGCGCTGGAACG--- 698  
|||  
Qy 715 ValLysValProLysGly---IleGlyLysLeuArgAspLeuGlnValLeuGluTyrVal 733  
|||  
Db 699 ---ATCCAGGTGGTGTATATGACGCTCACAATGCTGCAAGTTCTG---TACATG 749  
|||  
Qy 734 AspIleArgArgThrSerSerArgAla---IleLysGlu 745  
|||

750 GACCTCAGCTATGAGATTGGAAGGTTGGTGCAGTGGGAATGGTGTGATTTTCAGGAG 809  
|||  
Qy 746 LeuGlyGlnLeuSerLysLeuArgLysLeuGlyValThrThrAsnGlySerThrLysGlu 765  
|||  
Db 810 CTTGAGAGCCCTGCTAGGCTCAAGGCGCTGGACATCAACAATCT--- 857  
|||  
Qy 766 LysCysLysIleLeuTyrAlaAlaIleGluLysLeuSerSerLeuGlnSerLeuHisVal 785  
|||  
Db 858 ---GTTGAGGCTCTGGAGCGGCTCTCAGGCTATATCGCCTC--- 896  
|||  
Qy 786 AspAlaAlaGlyIleSerAspGlyThrLeuGluCysLeuAspSerIleSerPro 805  
|||  
Db 897 ---GCTGTTCCACAGAAACCTACTCATAAAGACATGCTCGAGCTTCAGAAAG--- 947  
|||  
Qy 806 ProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGluGluMetPro---Asn 823  
|||  
Db 948 ---ATAGAGCTTCTTCCAGCAAC 968  
|||  
Qy 824 TrpIleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeu--- 837  
|||  
Db 969 CTGTGGAAGACATGACTTAACCTGAGAGGGTGTGGATTGTCTGAGTCGCGCACTTAGCT 1028  
|||  
Qy 838 ---ArgSerLys 840  
|||  
Db 1029 GAGGTAATCATGATAGCAGCAAAAGAGCTGTGATAGCAATGCGCTTCCCGTTCCATC 1088  
|||  
Qy 841 LeuLysGluGlyLysThrMetLeu---IleLeuGlyAlaLeuProAsn 855  
|||  
Db 1089 TTGCAAGCTCGGGGGAACCTTGTGAGGAGAGACGACCTATCTTCCACCTTGCACGAT 1148  
|||  
Qy 856 LeuMetValLeuHisLeuTyrArgAsnAlaTyrLeuGlyGluLysLeuValPheLysThr 875  
|||  
Db 1149 ATCATCTTTCAGGCACTGTACAG---GTAAAGATCTCTACAAAGGC 1193  
|||  
Qy 876 GlyAla--- 877  
|||  
Db 1194 GGGTGTGTACAGAAATCTAGCATCTCTGTTTCTGTTATTCATGCGGTGGAGAGCTG 1253  
|||  
Qy 877 --- 877  
|||  
Db 1254 ATTACTGTTAGTGAAGAACAAGACATCGCGGCAAGCGGTGGCGAGGACAAGTTCCGCA 1313  
|||  
Qy 878 ---PheProAsnLeuArgThrLeuTrpIleTyrGluLeuAsp 890  
|||  
Db 1314 GGGTTTAGAGTCATCACACCTTCCCAACCTCAAGGAACCTGACTTCCATGCTTGGCA 1373  
|||  
Qy 891 GlnLeuArgGluIleArgPheGluAspGlySerSer---ProLeu 904  
|||  
Db 1374 AAGTTCCAGGAGCTC---AGCAGCAGCAGCATGTACTGCACTTCCCGCGG 1421  
|||  
Qy 905 LeuGluLysIleGluIleGlyGluCysArgLeuGluSerGlyIleThrGlyIleHis 924  
|||  
Db 1422 CTGGAGACCCCTGAAGATTATCGAGTGC--- 1448  
|||  
Qy 925 LeuProLysLeuLysGluIleProIleArgTyrGly 936  
|||  
Db 1449 ---CCGAATTTGAAGAAGCTGAAACTCTCAGCTGGG 1481  
|||

## RESULT 13

US-11-031-206-121  
; Sequence 121, Application US/11031206  
; Publication No. US20060031959A1  
; GENERAL INFORMATION:  
; APPLICANT: Rafaleki, Antoni  
; APPLICANT: Miao, Guo-Hua  
; APPLICANT: Falco, Saverio Carl  
; APPLICANT: Sakai, Hajime  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Odell, Joan T.  
; APPLICANT: Meyers, Blake  
; APPLICANT: Thorpe, Catherine  
; APPLICANT: Weng, Zude

; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in

; FILE REFERENCE: BB1357 US NA

; CURRENT APPLICATION NUMBER: US/11/031,206

; PRIOR FILING DATE: 2005-01-07

; PRIOR APPLICATION NUMBER: US/09/566,394

; PRIOR FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: 60/133038

; PRIOR FILING DATE: 1999-05-07

; PRIOR APPLICATION NUMBER: 60/133042

; PRIOR FILING DATE: 1999-05-07

; PRIOR APPLICATION NUMBER: 60/133427

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133437

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133428

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133438

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133436

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/137667

; PRIOR FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 208

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 121

; LENGTH: 795

; TYPE: DNA

; ORGANISM: Glycine max

US-11-031-206-121

Alignment Scores: 1.03e-10 Length: 795  
Pred. No.: 203.50 Matches: 51  
Score: 203.50 Conservative: 23  
Percent Similarity: 57.8% Mismatches: 51  
Best Local Similarity: 39.8% Indels: 3  
Query Match: 3.9% Gaps: 3  
DB:

US-10-656-394A-8 (1-1032) x US-11-031-206-121 (1-795)

QY 805 ProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGluGluMetProAsnTrp 824  
DB 8 CTTCTCAGTATCTCCAGCAGTATCTTGGTGGCGCTAGACATTTTCCCAATGG 67  
QY 825 IleGluGlnLeuThrHisLeuLysLysIleTyrLeuLeuArgSerLysLeuLysGluGly 844  
DB 68 ATAAGTTCTCTCAAGAAATTTGGTCCGAGTGTTCCTAAATGGAGCGGTTAGAGAG--- 124  
QY 845 LysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetValLeuHisLeuTyrArgAsn 864  
DB 125 GATCCTCTGGTACATCTTCAGANTTGGCAATCTAGACATCTTGAG--TTTCTTCA 181  
QY 865 AlaTyrLeuGlyGluLeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeu 884  
DB 182 GTTTATGTTGGTGCAGACATTCGATTTCAAGGCAAAAGGTTTCTAGTCTGAAGGTGTTA 241  
QY 885 TrpIleTyrGluLeuAspGluLeuIleArgPheGluAspGlySerSerProLeu 904  
DB 242 GGCCTGTGATTTAGATGGACTGAAATCAATGATCTGTGAGAGGAGGCATGCTGGT 301  
QY 905 LeuGluLysIleGluIleGlyGluCys---ArgLeuGluSerGlyIleThrGlyIlelle 923  
DB 302 CTTAAAGAGCTCATCATCAGCGCTGATTCATTGAAGCAGGATACCATTAGGCATTGAA 361  
QY 924 HisLeuProLysLeuGluIle 931  
DB 362 CACCTAACAAACTAATATCATATA 385

RESULT 14

US-11-031-206-123/c

; Sequence 123, Application US/11031206

; Publication No. US20060031959A1

; GENERAL INFORMATION:

; APPLICANT: Rafaleski, Antoni

; APPLICANT: Miao, Guo-Hua

; APPLICANT: Falco, Saverio Carl

; APPLICANT: Sakai, Hajime

; APPLICANT: Famodu, Omolayo O.

; APPLICANT: Odell, Joan T.

; APPLICANT: Meyers, Blake

; APPLICANT: Thorpe, Catherine

; APPLICANT: Weng, Zude

; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in

; FILE REFERENCE: BB1357 US NA

; CURRENT APPLICATION NUMBER: US/11/031,206

; PRIOR FILING DATE: 2005-01-07

; PRIOR APPLICATION NUMBER: US/09/566,394

; PRIOR FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: 60/133038

; PRIOR FILING DATE: 1999-05-07

; PRIOR APPLICATION NUMBER: 60/133042

; PRIOR FILING DATE: 1999-05-07

; PRIOR APPLICATION NUMBER: 60/133427

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133437

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133428

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133438

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/133436

; PRIOR FILING DATE: 1999-05-11

; PRIOR APPLICATION NUMBER: 60/137667

; PRIOR FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 208

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 123

; LENGTH: 306

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

NAME/KEY: unsure

LOCATION: (3)

FEATURE:

NAME/KEY: unsure

LOCATION: (146)

FEATURE:

NAME/KEY: unsure

LOCATION: (156)

FEATURE:

NAME/KEY: unsure

LOCATION: (172)

FEATURE:

NAME/KEY: unsure

LOCATION: (179)

FEATURE:

NAME/KEY: unsure

LOCATION: (219)

FEATURE:

NAME/KEY: unsure

LOCATION: (257)

FEATURE:

NAME/KEY: unsure

LOCATION: (272)

FEATURE:

NAME/KEY: unsure

LOCATION: (290)

FEATURE:

NAME/KEY: unsure

LOCATION: (294)

FEATURE:

NAME/KEY: unsure

LOCATION: (296-123)

US-11-031-206-123

Alignment Scores:

Pred. No.: 1.37e-09

Length: 306

Score:	187.00	Matches:	33
Percent Similarity:	61.5%	Conservative:	15
Best Local Similarity:	42.3%	Mismatches:	30
Query Match:	3.5%	Indels:	0
DB:	9	Gaps:	0

US-10-656-394A-8 (1-1032) x US-11-031-206-123 (1-306)

Qy	393	GluTrpGluLysPheTy rGluHisLeuProSerGluLeuLysLeuLeuProSerLeuGlu	412
Db	237	GAATGGGAAAAAATTAGGNGAACCTTAAGTTTCAGAGATGAACAAAGATCCCAATTAANT	178
Qy	413	AlaLeuArgArgMetValThrLeuGlyTy rAsnHisLeuProSerHisLeuLysProCys	432
Db	177	GGCATNACAAAGATTTTAGTGTTCAGTTTATGNTGATTTGCCATATTATCTGAATCATGC	118
Qy	433	PheLeuTy rLeuSerIleProGluAspPheGluLysLeuArgAsnArgLeuValGly	452
Db	117	TTATTGTATTTTGGTGATATCCCGAGACATATGAAGTTAACTCAAAAGATTAATTTGG	58
Qy	453	ArgTrpIleAlaGluGlyPheValArgProLysValGlyMetThrLysAsp	470
Db	57	CAATCGATACCTCAAGATTTCTGTAAGAGGAAGGAAGCAAAACATTATGAGGCAC	4

## RESULT 15

```

US-11-031-206-119
Sequence 119, Application US/11031206
Publication No. US20060031959A1
GENERAL INFORMATION:
APPLICANT: Rafalski, Antoni
APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
APPLICANT: Sakai, Hajime
APPLICANT: Famodu, Omolayo O.
APPLICANT: Odell, Joan T.
APPLICANT: Meyers, Blake
APPLICANT: Thorpe, Catherine
APPLICANT: Weng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
TITLE OF INVENTION: Stress Response
FILE REFERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/11/031,206
CURRENT FILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: US/09/566.394

```

```

; CURRENT AFFIDAVIT NUMBER: 00/11/0021/13
; CURRENT FILING DATE: 2005-01-07
: PRIOR APPLICATION NUMBER: US/09/566,394

```

805	ProProLeuLeuArgThrLeuValLeuAspGlyIleLeuGluGluMetProAsnTrp	824
Qy		
Db		
1	CTCTCTCAGTATCTCCAGCAGTTATCTTGGTGGGCGTCTAGACAATTTCCCAATGG	60
Qy		
Db		
825	IleGluGlnLeuThrHisLeuLysIleTyrlleuLeuArgSerIysLeuGly	844
Qy		
Db		
61	ATAAGTTCTCTCAAGATTTGGTCCGAGTGTTCATAAATGGAGCCGGTTAGAGAG---	117
Qy		
Db		
845	LysThrMetLeuIleLeuGlyAlaLeuProAsnLeuMetValLeuHisLeuTyrlArgAsn	864
Qy		
Db		
118	GATCCTCTGGTACATCTTCAAGATTTGCCAAATCTAAGACATCTTGAG---TTTCTTCAA	174
Qy		
Db		
865	AlaTyrlLeuGlyGluLysLeuValPheLysThrGlyAlaPheProAsnLeuArgThrLeu	884
Qy		
Db		
175	GTTATGTTGGTGAGACATTGCATTTCAAGCAAAAGGGTTTCTCTAGTCTGAAGGTGTTA	234
Qy		
Db		
885	TrpIleTyrlGluLeuAspGlnLeu-ArgGluIleArgPheGluAspGlySerProLe	904
Qy		
Db		
235	GGCCTTGATGATTTAGATGGACTGGAAATCAATGACTGTGGAGAGGGAGCAATGCTGTG	294
Qy		
Db		
904	uLeuGluLysIleGluIleGlyGluCys---ArgLeuGluSerGlyIleThrGlyIle1	923
Qy		
Db		
295	TCTTAAANAAGCTCATCATCCAGCGCTGTGATTTCATTGGAAGCAGGTACCATAGGCATTGA	354
Qy		
Db		
923	eHisLeuProLysLeuLys	929
Qy		
Db		
355	ACACCTAAACAAAACATAAAA	373
Qy		
Db		



Mon Mar 13 10:28:19 2006

us-10-656-394a-8.p2n.rnpbn

Page 18

Search completed: March 9, 2006, 23:56:55  
Job time : 2304 secs